

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 00:38:30 ; Search time 2211 Seconds

(without alignments)
10609.164 Million cell updates/sec

Title: US-09-966-881-13

Perfect score: 806
Sequence: 1 TGTTCCTCCTCTGATCACA.....TCCCTTCCTCATGATG 806

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: 1: gb_ba: 2: gb_hlg: 3: gb_in: 4: gb_om: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_sts: 12: gb_sy: 13: gb_un: 14: gb_vl: 15: em_ba: 16: em_fun: 17: em_hum: 18: em_in: 19: em_mu: 20: em_om: 21: em_or: 22: em_ov: 23: em_pat: 24: em_ph: 25: em_pl: 26: em_ro: 27: em_sts: 28: em_un: 29: em_vl: 30: em_hlg_hum: 31: em_hlg_inv: 32: em_hlg_other: 33: em_hlg_mus: 34: em_hlg_pla: 35: em_hlg_rod: 36: em_hlg_mam: 37: em_hlg_vrt: 38: em_sy: 39: em_hlgo_hum: 40: em_hlgo_mus: 41: em_hlgo_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	778	96.5	806	6 A70152	A70152 Sequence 13
2	612.4	76.0	1788	6 AF206320	AF206320 Musa acun
3	591.8	73.4	748	6 A83011	A83011 Sequence 18
4	591.2	73.3	745	6 A83004	A83004 Sequence 11
5	588.8	73.1	793	6 A83001	A83001 Sequence 8
6	588.8	73.1	793	6 MA299965	299965 Musa acumin
7	572.2	71.0	727	6 A83014	A83014 Sequence 21
8	543.8	67.5	727	6 A70155	A70155 Sequence 16
9	536	66.5	724	6 A70157	A70157 Sequence 18
10	510.8	63.4	704	6 A83000	A83000 Sequence 7
11	496.8	61.6	706	6 A83012	A83012 Sequence 19
12	174.4	21.6	127202	2 OSJN00272	AL731627 Oryza sat
13	169.4	21.0	1633	8 AY085026	AY085026 Arabidops
14	152	18.9	90142	8 ATAC016827	AC016827 Arabidops
15	151	18.7	823	6 A83003	A83003 Sequence 10
16	150	18.6	1408	8 EX063550	U63550 Fragaria x
17	148	18.4	1523	8 AY086099	AY086099 Arabidops
18	144.8	18.0	1496	8 AF206319	AF206319 Musa acun
19	144.4	17.9	749	6 A82999	A82999 Sequence 6
20	143.2	17.8	1462	8 MAPEL	X92943 M.acuminata
21	142.8	17.7	842	6 A70156	A70156 Sequence 17
22	141.4	17.5	708	6 A83002	A83002 Sequence 9
23	141	17.5	1525	8 AY050404	AY050404 Arabidops
24	141	17.5	1556	8 AY050795	AY050795 Arabidops
25	134.6	16.7	687	6 A70153	A70153 Sequence 14
26	134.6	16.7	687	6 MA299977	299977 Musa acumin
27	133.2	16.5	5368	8 AF339024	AF339024 Fragaria
28	131.6	16.3	772	6 A83010	A83010 Sequence 17
29	131.6	16.3	772	6 MA299970	299970 Musa acumin
30	131	16.3	758	6 A83005	A83005 Sequence 12
31	130.4	16.2	1431	8 AY058197	AY058197 Arabidops
32	129.2	16.0	794	6 A83006	A83006 Sequence 13
33	128.8	16.0	728	6 A83013	A83013 Sequence 20
34	128.4	15.9	745	6 A83008	A83008 Sequence 15
35	127.2	15.8	1782	8 AY087724	AY087724 Arabidops
36	127	15.8	1065	8 AY066033	AY066033 Arabidops
37	127	15.8	1459	8 AY065034	AY065034 Arabidops
38	127	15.8	1788	8 AY054200	AY054200 Arabidops
39	126.2	15.7	731	6 A83009	A83009 Sequence 16
40	124	15.4	1440	6 AX005936	AX005936 Sequence
41	124	15.4	1440	6 ZEPCLY	Y09541 Z.elegans m
42	123.6	15.3	4143	8 AF339025	AF339025 Fragaria
43	122.6	15.2	100079	8 TIG11	AC002376 Sequence
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ALIGNMENTS

RESULT 1
A70152 LOCUS 806 bp DNA linear PAT 07-MAY-1999
DEFINITION Sequence 13 from Patent WO9811228.
ACCESSION A70152
VERSION A70152.1 GI:4774567
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 806)
AUTHORS Seymour G.B., Bird C.R. and Medina-Suarez, R.D.
TITLE GENETIC CONTROL OF FRUIT RIPENING
PATENT: WO 9811228-A 13 19-MAR-1998;
JOURNAL SEYMOUR GRAHAM BARRON (GB)

FEATURES
Source Location/Qualifiers
1..806
/organism="unidentified"
/db_xref="taxon:32644"
/clone="U-068"

BASE COUNT 157 a 229 c 212 g 180 t 28 others

Query Match 96.5%; Score 778; DB 6; Length 806;
Best Local Similarity 100.0%; Pred. No. 3.8e-133;
Matches 806; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TGTTCCTCCTCCATCATCTTTTGTCTGCGAAGAGTGAAGAGGAGGCG 60
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1 TGTTCCTCCTCCATCATCTTTTGTCTGCGAAGAGTGAAGAGGAGGCG 60

61 GCAATGACGGCGGTTTAAGATGATTCCTCTGCTCTCTCTCTCTCTCTG 120
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61 GCAATGACGGCGGTTTAAGATGATTCCTCTGCTCTCTCTCTCTCTCTG 120

121 CTGCTTTGAACGAGGTGCGGGGTGATTTGGAACGAGAGTCTCTGCTGAG 180
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181 GCGGAGATCGCGGAGGAGCTTGAAGAGGCTCGGGAACGAGAGTCTCTG 240
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421 GTCAACAGAAAAAGCTGCTGACTGCGGAGTGGCTTTGAGCGACGCAAT 480
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481 CGCGAGCGGAGTGGCTGCTGACTGCGGAGTGGCTTTGAGCGACGCAAT 540
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481 CGCGAGCGGAGTGGCTGCTGACTGCGGAGTGGCTTTGAGCGACGCAAT 540

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541 GCGCGAGCGGAGTGGCTGCTGACTGCGGAGTGGCTTTGAGCGACGCAAT 600

601 AAACNCAANTGAAATCTCNCCTCANGAAGAACTCTTATGAACAGCTTAA 660
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601 AAACNCAANTGAAATCTCNCCTCANGAAGAACTCTTATGAACAGCTTAA 660

661 CGATGAGACNCGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
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661 CGATGAGACNCGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720

721 TCCCAACNCT 780
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721 TCCCAACNCT 780

781 CCCCNCCT 806
|||||
781 CCCCNCCT 806

RESULT 2 AF206320 1788 bp mRNA linear PLN 21-DEC-1999
LOCUS AF206320
DEFINITION Musa acuminata pectate lyase 2 (PL2) mRNA, complete cds.

ACCESSION AF206320
VERSION AF206320.1 GI:6606533
KEYWORDS
SOURCE Musa acuminata
ORGANISM Musa acuminata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
Musa.

REFERENCE 1 (bases 1 to 1788)
Ong,C.R., Pua,E.C. and Liu,P.
Molecular cloning and characterization of pectate lyase in banana
Unpublished
2 (bases 1 to 1788)
Ong,C.R., Pua,E.C. and Liu,P.
Direct Submission
Submitted (18-NOV-1999) Department of Biological Sciences, National
University of Singapore, 10 Kent Ridge Crescent, Singapore 119260

FEATURES
source Location/Qualifiers
1..1788
/organism="Musa acuminata"
/cultivar="Williams"
/db_xref="taxon:4641"
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78..1442
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GSGNPIDDCWDPMHVRKRLADCGGIFRMAIGDGLYVVTGGDDPVNPR
GLRAYAIDVDPLMTFEKDMETLKEELINSEFTIDRGVNHIAAGACITLOYIT
NVILGHILHOCKPGNMAVRSRPSHWRPMADGDAYISFGSHIWDHGLSNCAD
GLVAYMSTALIVSYNNMFTVHNEMVLLGHDSYRDSIMQVTLAFNFGSLGRNP
RCRCHRYVYVNDTTHREMYAIGSANPTINSQRRYLAIPNPAKEVTKAVDIDST
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BASE COUNT 419 a 473 c 470 g 426 t

Query Match 76.0%; Score 612.4; DB 8; Length 1788;
Best Local Similarity 88.6%; Pred. No. 1e-149;
Matches 716; Conservative 0; Mismatches 82; Indels 10; Gaps 6;

1 TGTTCCTCCTCCATCATCTTTTGTCTGCGAAGAGTGAAGAGGAGGCG 60
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15 TGTTCCTCCTCCATCATCTTTTGTCTGCGAAGAGTGAAGAGGAGGCG 74

61 GCAATGACGGCGGTTTAAGATGATTCCTCTGCTCTCTCTCTCTCTCTG 120
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75 GCAATGACGGCGGTTTAAGATGATTCCTCTGCTCTCTCTCTCTCTCTG 134

121 CTGCTTTGAACGAGGTGCGGGGTGATTTGGAACGAGAGTCTCTGCTGAG 180
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135 CTGCTTTGAACGAGGTGCGGGGTGATTTGGAACGAGAGTCTCTGCTGAG 194

181 GCGGAGATCGCGGAGGAGCTTGAAGAGGCTCGGGAACGAGAGGCGGAG 240
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195 GCGGAGATCGCGGAGGAGCTTGAAGAGGCTCGGGAACGAGAGGCGGAG 254

241 TCCTTGAAGAGAGGCTGTAAACCGCGGAGAGGCGAGTGCAGAGCCGAG 300
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255 TCCTTGAAGAGAGGCTGTAAACCGCGGAGAGGCGAGTGCAGAGCCGAG 314

301 GTTCTTGAAGAGGCTGTAAACCGCGGAGAGGCGAGTGCAGAGCCGAG 360
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315 GTTCTTGAAGAGGCTGTAAACCGCGGAGAGGCGAGTGCAGAGCCGAG 374

361 CTGCTGCGGCTTGAAGAGGCTGTAAACCGCGGAGAGGCGAGTGCAGAG 420
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375 CTGCTGCGGCTTGAAGAGGCTGTAAACCGCGGAGAGGCGAGTGCAGAG 434

QY 421 GTCACAGAAAAAGCTGCTGACTGCGGCAATTGGCTTTGGACGCAACGCMATANGTGC 480
DB 435 GTCACAGAAAAAGCTGCTGACTGCGGCAATTGGCTTTGGACGCAACGCMATANGTGC 494
QY 481 CGGAGCGGGAATTTGCTGCTTGTGACAGACTCCGGGACMANGATCCCGTGAATCTC 540
DB 495 CGGAGCGGGAATTTGCTGCTTGTGACAGACTCCGGGACMANGATCCCGTGAATCTC 552
QY 541 GCCCGGGAACCTTANATACCCGTCNTCCANANGAATGGCCCTCTGGGATCCCTTT 600
DB 553 GCCCGGGAACCTTANATACCCGTCNTCCANANGAATGGCCCTCTGGGATCCCTTT 608
QY 601 AAACNCAANTGGAATCTCNCNANGAAGAACTCMTTATGAACAGCTTTAAMACMAT 660
DB 609 AAACNCAANTGGAATCTCNCNANGAAGAACTCMTTATGAACAGCTTTAAMACMAT 667
QY 661 CGATGAGCNCNGTCTGCTGCTGCAACATGGCAATGGGCGCTGCTGCAACNCAATTCN 720
DB 668 CGATGAGCNCNGTCTGCTGCTGCAACATGGCAATGGGCGCTGCTGCAACNCAATTCN 726
QY 721 TCCCAACACNTCTTCTCCNTNGCTCCNC--TCCCAATGCAACCCNCGGAATTCCTN 778
DB 727 TCAACAGCTCATCATCATCATGCGCTCCACATCCAGCTGCAAGCCACCGGGAATCCA 786
QY 779 GTCCCCNCTGCCCTTCTCTCTATGGATNG 806
DB 787 TGGTCCGACAGCTCTCTCTCTACTATGG 814

RESULT 3
LOCUS AB3011 748 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 18 from Patent WO9853085.
ACCESSION AB3011
VERSION AB3011.1 GI:6732491
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 748)
AUTHORS Seymour G.B. and Bird C.R.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL Patent: WO 9853085-A 18 26-NOV-1998;
SEYMOUR GRAHAM BARRON (GB); ZENECA LTD (GB)
FEATURES
source 1..748
location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/clone="U-113"
BASE COUNT 154 a 211 c 206 g 163 t 14 others
ORIGIN

Query Match 73.4%; Score 591.8; DB 6; Length 748;
Best Local Similarity 91.7%; Pred. No. 2.5e-144;
Matches 664; Conservative 0; Mismatches 52; Indels 8; Gaps 4;

QY 1 TGTTCCTCCTTGATGATCATCTTTTGTCTGTGGAAACGTGAGAGTGAGAGAGCG 60
DB 16 TGTTCCTCCTTGATGATCATCTTTTGTCTGTGGAAACGTGAGAGTGAGAGAGCG 75
QY 61 GCAATGACGGCGGGTTTAAGATGATCTCTCTGCTTCTTCTTCTGGGCTTCG 120
DB 76 GCAATGACGGCGGGTTTAAGATGATCTCTCTGCTTCTTCTTCTGGGCTTCG 135
QY 121 CTGCTTTGAACGAGAGTGCGGGGTGATTTGAAGCAGAGGTCCTTGCTGAGGAAT 180
DB 136 CTGCTTTGAACGAGAGTGCGGGGTGATTTGAAGCAGAGGTCCTTGCTGAGGAAT 195
QY 181 GCGGAGACATCGCGGAGAGCTTGAGAGAGGCTCCGGAACGAGACGAGCGGATGCT 240
DB 196 GCGGAGACATCGCGGAGAGCTTGAGAGAGGCTCCGGAACGAGACGAGCGGATGCT 255

QY 241 TCTTGGAGAGAGGCTGTAAACCCGGGACAGAAACCCGAGTGAAGACCCCGAGAG 300
DB 256 TCTTGGAGAGAGGCTGTAAACCCGGGACAGAAACCCGAGTGAAGACCCCGAGAG 315
QY 301 GTTGCTTGAACGGTCTGATGACATTAATCAACAGCAGGCTGCGAGATCTTTGGTAT 360
DB 316 GTTGCTTGAACGGTCTGATGACATTAATCAACAGCAGGCTGCGAGATCTTTGGTAT 375
QY 361 CTGCTGCTGCTGACGCAACCCGATGAGACTGCTGGGCGTGGCCAGCTGATGGCAT 420
DB 376 CTGCTGCTGCTGACGCAACCCGATGAGACTGCTGGGCGTGGCCAGCTGATGGCAT 435
QY 421 GTCACAGAAAAAGCTGCTGACTGCGGCAATTGGCTTTGGACGCAACGCMATANGTGC 480
DB 436 GTCACAGAAAAAGCTGCTGACTGCGGCAATTGGCTTTGGACGCAACGCMATANGTGC 495
QY 481 CGGAGCGGGAATTTGCTGCTTGTGACAGACTCCGGGACMANGATCCCGTGAATCTC 540
DB 496 CGGAGCGGGAATTTGCTGCTTGTGACAGACTCCGGGACMANGATCCCGTGAATCTC 555
QY 541 GCCCGGGAACCTTANATACCCGTCNTCCANANGAATGGCCCTCTGGGATCCCTTT 600
DB 556 GCCCGGGAACCTTANATACCCGTCNTCCANANGAATGGCCCTCTGGGATCCCTTT 610
QY 601 AAACNCAANTGGAATCTCNCNANGAAGAACTCMTTATGAACAGCTTTAAMACMAT 660
DB 611 AAACNCAANTGGAATCTCNCNANGAAGAACTCMTTATGAACAGCTTTAAMACMAT 669
QY 661 CGATGAGCNCNGTCTGCTGCTGCAACATGGCAATGGGCGCTGCTGCAACNCAATTCN 720
DB 670 CGATGAGCNCNGTCTGCTGCTGCAACATGGGCGCTGCTGCAACNCAATTCN 727
QY 721 TCCC 724
DB 728 CACC 731

RESULT 4
LOCUS AB3004 745 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 11 from Patent WO9853085.
ACCESSION AB3004
VERSION AB3004.1 GI:6732484
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 745)
AUTHORS Seymour G.B. and Bird C.R.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL Patent: WO 9853085-A 11 26-NOV-1998;
SEYMOUR GRAHAM BARRON (GB); ZENECA LTD (GB)
FEATURES
source 1..745
location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
/clone="U-52"
BASE COUNT 153 a 204 c 203 g 163 t 22 others
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Query Match 73.3%; Score 591.2; DB 6; Length 745;
Best Local Similarity 90.5%; Pred. No. 3.7e-144;
Matches 673; Conservative 0; Mismatches 61; Indels 10; Gaps 5;

QY 1 TGTTCCTCCTTGATGATCATCTTTTGTCTGTGGAAACGTGAGAGTGAGAGAGCG 60
DB 7 TGTTCCTCCTTGATGATCATCTTTTGTCTGTGGAAACGTGAGAGTGAGAGAGCG 66
QY 61 GCAATGACGGCGGGTTTAAGATGATCTCTCTGCTTCTTCTTCTGGGCTTCG 120
DB 67 GCAATGACGGCGGGTTTAAGATGATCTCTCTGCTTCTTCTTCTGGGCTTCG 126
QY 121 CTGCTTTGAACGAGAGTGCGGGGTGATTTGAAGCAGAGGTCCTCTGCTGAGGAAT 180

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Db      127 CTGGTTTGAACGAGGTGGGGGTGATGGAGAGAGGTCTCTGGCTGAGGAAT 186
Oy      181 GGGGAGATCGCGGAGAGAGCTTTGAGAGAGGCTCCGCGAAGCGGACCGCCGATGCT 240
Db      187 GGGGAGATCGCGGAGAGAGCTTTGAGAGAGGCTCCGCGAAGCGGACCGCCGATGCT 246
Oy      241 TCTTTGGAAGAGAGGCTGTAAACCGGCGCAGAGAACCGCGAGTCAGACGCCCGAGAG 300
Db      247 TCTTTGGAAGAGAGGCTGTAAACCGGCGCAGAGAACCGCGAGTCAGACGCCCGAGAG 306
Oy      301 GTTGTGTGAGGCTGTGATGACCAATCAACACAGCGCTCGAGATCTTTGGTAT 360
Db      307 GTTGTGTGAGGCTGTGATGACCAATCAACACAGCGCTCGAGATCTTTGGTAT 366
Oy      361 CTGTGTCGCGGTTTCAGGCAACCGGATCGACGCTGTGGCGGTGGACCTGATTGGCAT 420
Db      367 CTGTGTCGCGGTTTCAGGCAACCGGATCGACGCTGTGGCGGTGGACCTGATTGGCAT 426
Oy      421 GTCAACAG-AAAAAAGCTGCTGACTGGCGCATTTGGAGCGCAACGCAATANGTG 479
Db      427 GTCAACAGAAAAAAGCTGCTGACTGGCGCATTTGGAGCGCAACGCAATANGTG 486
Oy      480 CCGCAGCGGGAATTTGTTGTTGTGACAGACTCCGGGAGCAATGATCCCGTGAATCT 539
Db      487 CCGCAGCGGGA-ANTTGTACGTTGTGACAGACTCCGGGAGCAATGAT-CCGCTGAATCT 544
Oy      540 CGCCCGGGAACACTTAAATACCCCGTCNTCCAAANGAAGTTGCCCTCTGGATCCCTT 599
Db      545 CCGCGGGAACNCTTAAATACCGCTGATCC-ANGACGTGCCCTCTGATCACCCTT 600
Oy      600 TAAACNCAANTGAAATCTCNCNTCANGAAGAACTCTTATGAACAGC---TTTANA 656
Db      601 TAAACNCAANTGAAATCTCNCNTCANGAAGAACTCTTATGAACAGC---TTTANA 660
Oy      657 CNATGATGAGCNCNGTCTGCTGCTGACATTCGCAATGGCGCTGCTGATCAGCAAT 716
Db      661 ACATGATGAGCNCNGTCTGCTGCTGACATTCGCAATGGCGCTGCTGATCAGCAAT 720
Oy      717 TTCNTCCCAACNTCTCTCCCT 740
Db      721 TACATCACCAACGTCATCTCCAT 744

RESULT 5
AB3001      AB3001      793 bp      DNA      linear      PAT 21-JAN-2000
DEFINITION      Sequence 8 from Patent WO9853085.
ACCESSION      AB3001.
VERSION      AB3001.1 GI:6732481
KEYWORDS
SOURCE      unidentified.
ORGANISM      unidentified.
REFERENCE      1 (bases 1 to 793)
AUTHORS      Seymour,G.B. and Bird,C.R.
TITLE      GENETIC CONTROL OF FRUIT RIPENING
JOURNAL      Patent: WO 9853085-A 8 26-NOV-1998;
SEYMOUR GRAHAM BARON (GB); ZENECA LTD (GB)
FEATURES
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ORIGIN
Query Match      73.1%; Score 588.8; DB 6; Length 793;
Best Local Similarity 88.7%; Pred.No.1.6e-143;
Matches 705; Conservative 0; Mismatches 77; Indels 13; Gaps 7;
Oy      1 TGTTCCTCTCCATCATCTTTTGTCTGGAAGCTGAGAGTGAAGAGGCG 60
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Oy      61 GCATAGAGCGCGGTTTAAAGATGATTCCTCTGCTCTCTCTCTCTCTCTCTCTG 120
Db      68 GCATAGAGCGCGGTTTAAAGATGATTCCTCTGCTCTCTCTCTCTCTCTCTCTG 127
Oy      121 CTGTTTGAACGAGAGCTGGGGGTGATTTGAACGAGAGGCTCTCTGCTGAGGAT 180
Db      128 CTGTTTGAACGAGAGCTGGGGGTGATTTGAACGAGAGGCTCTCTGCTGAGGAT 187
Oy      181 GGGGAGATCGCGGAGAGGCTTTGAGAGAGGCTCCGGAACCGGACCGCCGATGCT 240
Db      188 GGGGAGATCGCGGAGAGGCTTTGAGAGAGGCTCCGGAACCGGACCGCCGATGCT 247
Oy      241 TCTTTGGAAGAGAGGCTGTAAACCGGCGCAGAGAGCGCGAGTCAGACGCCCGAGAG 300
Db      248 TCTTTGGAAGAGAGGCTGTAAACCGGCGCAGAGAGCGCGAGTCAGACGCCCGAGAG 307
Oy      301 GTTGTGTGAGGCTGTGATGACCAATCAACACAGCGCTCGAGATCTTTGGTAT 360
Db      308 GTTGTGTGAGGCTGTGATGACCAATCAACACAGCGCTCGAGATCTTTGGTAT 367
Oy      361 CTGTGTCGCGGTTTCAGGCAACCGGATCGACGCTGTGGCGGTGGACCTGATTGGAT 420
Db      368 CTGTGTCGCGGTTTCAGGCAACCGGATCGACGCTGTGGCGGTGGACCTGATTGGAT 427
Oy      421 GTCAACAG-AAAAAAGCTGCTGACTGGCGCATTTGGAGCGCAACGCAATANGTG 479
Db      428 GTCAACAGAAAAAAGCTGCTGACTGGCGCATTTGGAGCGCAACGCAATANGTG 487
Oy      480 CCGCAGCGGGAATTTGTTGTTGTGACAGACTCCGGGAGCAATGATCCCGTGAATCT 539
Db      488 CCGCAGCGGGA-ANTTGTGCTGTGACAGACTCCGGGAGCAATGATCCCGTGAATCT 546
Oy      540 CGCCCGGGAACACTTAAATACCCCGTCNTCCAAANGAAGTTGCCCTCTGGATCCCTT 599
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Oy      600 TAAACNCAANTGAAATCTCNCNTCANGAAGAACTCTTATGAACAGCTTTAANCA 659
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Oy      660 TCGATGAGCNCNGTCTCTGCTGCTGACATTCGCAATGGCGCTGCTGATCAGCAAT 719
Db      661 TCGATGAGCNCG--GTGACGTCTCAGATTCGCAATGGCGCTGCTGATCAGCAAT 717
Oy      720 TTCCTCAACNTCTCTCTCNCNTGCTCCNCT--CCCAATGCAACCGCGGAATTCCT 777
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Oy      778 NGTCCCGCTCCCT 792
Db      778 TGTTCCTCTCTCTCT 792

RESULT 6
MA29965      MA29965      793 bp      mRNA      linear      PLN 03-NOV-1999
DEFINITION      Musa acuminata mRNA for putative pectate lyase (type I) (clone PBAN
ACCESSION      MA29965.
VERSION      MA29965.1 GI:6249483
KEYWORDS
SOURCE      Musa acuminata.
ORGANISM      Musa acuminata.
REFERENCE      1 (bases 1 to 793)
AUTHORS      Drury,R., Hortensteiner,S., Donison,I., Bird,C.R. and Seymour,G.B.
TITLE      Chlorophyll catabolism and gene expression in the peel of ripening
JOURNAL      Physiol. Plantarum 107, 32-38 (1999)

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REFERENCE 2 (bases 1 to 793)
AUTHORS Medina-Suarez, R.
TITLE Direct Submission
JOURNAL Submitted (17-OCT-1997) R. Medina-Suarez, Horticulture Research International, Wellesbourne, Warwick, CV35 9EF, UNITED KINGDOM

FEATURES
source location/Qualifiers
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/cultivar="Grand Nain"
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/product="pectate lyase (type I)"
/note="putative"

BASE COUNT 170 a 222 c 215 g 171 t 15 others

ORIGIN

Query Match 73.1%; Score 588.8; DB 8; Length 793;
Best Local Similarity 88.7%; Pred. No. 1.6e-143;
Matches 705; Conservative 0; Mismatches 77; Indels 13; Gaps 7;

QY 1 TGTTCCTCCTTCGATCACAATCTTTTGTCTCTGGGAAACGTGAGAGGTGAGAGGGCG 60
DB 8 TGTTCCTCCTTCGATCACAATCTTTTGTCTCTGGGAAACGTGAGAGGTGAGAGGGCG 67

QY 61 GCATAGACGGGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 120
DB 68 GCATAGACGGGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 127

QY 121 CTGGTTTGAACGGAGGTGCGGGGGTGGATTGGAAGCAGAGAGTCTCTCTCTCTCTCTCTG 180
DB 128 CTGGTTTGAACGGAGGTGCGGGGGTGGATTGGAAGCAGAGAGTCTCTCTCTCTCTCTCTG 187

QY 181 GCGGAGCATCGCGAGAGCTTGAGAGAGCCTCCGGAACGGCAGCAGCGCCGATGCT 240
DB 188 GCGGAGCATCGCGAGAGCTTGAGAGAGCCTCCGGAACGGCAGCAGCGCCGATGCT 247

QY 241 TCCTTGGAAGAGAGGCTGTACCCGGGAGCAGAAAGCCGAGTCGACGACCCGAGAG 300
DB 248 TCCTTGGAAGAGAGGCTGTACCCGGGAGCAGAAAGCCGAGTCGATGACCCGAGAG 307

QY 301 GTTGCTTCGACGGTCTCTGATGACCATATATCAACAGCAGCGCTGCGACATCTCTGTTAT 360
DB 308 GTTGCTTCGACGGTCTCTGATGACCATATATCAACAGCAGCGCTGCGACATCTCTGTTAT 367

QY 361 CTGTCTGCGGTTTCAGGCAACCGGATGAGAGTCTGCGGTGCGACCTGATGGCAT 420
DB 368 CTGTCTGCGGTTTCAGGCAACCGGATGAGAGTCTGCGGTGCGACCTGATGGCAT 427

QY 421 GTCAACAG-AAAAAGCTGCTGACTGCGGCAATGGTTTGAACGCAACGANTANGTG 479
DB 428 GTCAACAGAAAAAGCTGCTGACTGCGGCAATGGTTTGAACGCAACGANTANGTG 487

QY 480 CCGGAGAGGGAATTTGTTGTTGAGACACTCCGGGAGCAGATGATCCCGTGAATCT 539
DB 488 CCGGAGAGGAG-ANTGTGCTGTTGACAGACTCCGGGAGCAGATGATCCCGTGAATCT 546

QY 540 CCGGAGAGGGAATTTGTTGTTGAGACACTCCGGGAGCAGATGATCCCGTGAATCT 599
DB 547 CCGGAGAGGGAATTTGTTGTTGAGACACTCCGGGAGCAGATGATCCCGTGAATCT 602

QY 600 TAAACNANANGGAATCTCNCNANGAAGAACTNTATGAACAGCTTAAACNA 659
DB 603 TAAACNANANGGAATCTCNCNANGAAGAACTNTATGAACAGCTTAAACNA 660

QY 660 TCGATGAGACNCTGCTCTGTCACATTCGCAATGGCGCTGCTTACCAATTC 719
DB 661 TCGATGAGACNCTGCTCTGTCACATTCGCAATGGCGCTGCTTACCAATTC 717

QY 720 NTCCCAACNTCTTCTCTCCTNCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 777

DB 718 ATCACCAACATCATCTGAGCTCCAGTCCACAAAGCAGAACCCAGCAGATTCCT 777

QY 778 NTGCCCCNCTCCCT 792

DB 778 TGTGCCCATCTCTT 792

RESULT 7
AB3014
LOCUS
DEFINITION Sequence 21 from Patent WO9853085.
ACCESSION AB3014
VERSION AB3014.1 GI:6732494
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 727)
AUTHORS Seymour, G.B. and Bird, C.R.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL PATENT: WO 9853085-A 21 26-NOV-1998;
SEYMOUR GRAHAM BARON (GB); ZENECA LTD (GB)
FEATURES
source location/Qualifiers
1..727
/organism="unidentified"
/db_xref="taxon:32644"
/clone="U-139"

BASE COUNT 144 a 199 c 202 g 157 t 25 others

ORIGIN

Query Match 71.0%; Score 572.2; DB 6; Length 727;
Best Local Similarity 90.9%; Pred. No. 3.5e-139;
Matches 653; Conservative 0; Mismatches 57; Indels 8; Gaps 5;

QY 1 TGTTCCTCCTTCGATCACAATCTTTTGTCTCTGGGAAACGTGAGAGGTGAGAGGGCG 60
DB 16 TGTTCCTCCTTCGATCACAATCTTTTGTCTCTGGGAAACGTGAGAGGTGAGAGGGCG 75

QY 61 GCATAGACGGGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 120
DB 76 GCATAGACGGGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 135

QY 121 CTGGTTTGAACGGAGGTGCGGGGGTGGATTGGAAGCAGAGAGTCTCTCTCTCTCTCTCTG 180
DB 136 CTGGTTTGAACGGAGGTGCGGGGGTGGATTGGAAGCAGAGAGTCTCTCTCTCTCTCTCTG 195

QY 181 GCGGAGCATCGCGAGAGCTTGAGAGAGCCTCCGGAACGGCAGCAGCGCCGATGCT 240
DB 196 GCGGAGCATCGCGAGAGCTTGAGAGAGCCTCCGGAACGGCAGCAGCGCCGATGCT 255

QY 241 TCCTTGGAAGAGAGGCTGTACCCGGGAGCAGAAAGCCGAGTCGACGACCCGAGAG 300
DB 256 TCCTTGGAAGAGAGGCTGTACCCGGGAGCAGAAAGCCGAGTCGACGACCCGAGAG 315

QY 301 GTTGCTTCGACGGTCTCTGATGACCATATATCAACAGCAGCGCTGCGACATCTCTGTTAT 360
DB 316 GTTGCTTCGACGGTCTCTGATGACCATATATCAACAGCAGCGCTGCGACATCTCTGTTAT 375

QY 361 CTGTCTGCGGTTTCAGGCAACCGGATGAGAGTCTGCGGTGCGACCTGATGGCA 419
DB 376 CTGTCTGCGGTTTCAGGCAACCGGATGAGAGTCTGCGGTGCGACCTGATGGCA 435

QY 420 TGTCAACAGAAAAAGCTGCTGACTGCGGCAATGGTTTGAACGCAACGANTANGTG 479
DB 436 TGTCAACAGAAAAAGCTGCTGACTGCGGCAATGGTTTGAACGCAACGANTANGTG 495

QY 480 CCGGAGAGGGAATTTGTTGTTGAGACACTCCGGGAGCAGATGATCCCGTGAATCT 539
DB 496 CCGGAGAGGGAATTTGTTGTTGAGACACTCCGGGAGCAGATGATCCCGTGAATCT 554

QY 540 CCGGAGAGGGAATTTGTTGTTGAGACACTCCGGGAGCAGATGATCCCGTGAATCT 599

Db 555 CMCAGGAGACCTTANATAGCCGTCATCC---ANGACTNCCCCTCTGGTCACTTT 610
Qy 600 TAAACNCAANTGAAATCTCNCNTCANGAGAAGAACTCTTATGAACAGCTTTAANACNA 659
Db 611 TAAACNCAANTGAAATCTCNCNTCANGAGAAGAACTCTTATGAACAGCTTTAANACNA 669
Qy 660 TCGATGACNCGTCTCTCCCTCCGACATTGGCCATGGGCGCTGCTACACNCAATT 717
Db 670 TCGATGGAC-CCGTGTCAACGTTCCNCTGCGCAATGGGCGCTGCTACNCTCNCNNT 726

RESULT 8
A70155
LOCUS A70155 727 bp DNA linear PAT 07-MAY-1999
DEFINITION Sequence 16 from Patent W09811228.
ACCESSION A70155
VERSION A70155.1 GI:4774570
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 727)
AUTHORS Seymour,G.B., Bird,C.R. and Medina-Suarez,R.D.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL Patent: WO 9811228-A 16 19-MAR-1998;
SETMOUR GRAHAM BARON (GB)
FEATURES
source Location/Qualifiers
1..727
/organism="unidentified"
/db_xref="taxon:32644"
/clone="U-089"

BASE COUNT 145 a 205 c 196 g 159 t 22 others
ORIGIN
Query Match 67.5%; Score 543.8; DB 6; Length 727;
Best Local Similarity 86.6%; Pred. No. 9,8e-132;
Matches 628; Conservative 0; Mismatches 91; Indels 6; Gaps 4;

Qy 2 GTTCTCTCTTCGATCAGATCTTTTGGCTGGGAACGTGAGAGGTGAGAGAGGCGG 61
Db 8 GTTCTCTCTTCGATCAGATCTTTTGGCTGGGAACGTGAGAGGTGAGAGAGGCGG 67
Qy 62 CAATGAGGCGGTTAAGATGAGATTCCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 121
Db 68 CAATGAGGCGGTTAAGATGAGATTCCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 127
Qy 122 TGGTTTGAACGAGGTGGGGGTGATTGGAAGGAGAGAGTCTCTGCTGAGAGATG 181
Db 128 TGGTTTGAACGAGAGTGGGGGTGATTGGAAGGAGAGAGTCTCTGCTGAGAGATG 187
Qy 182 GCGGAGCATGCGGAGGAGCTTGAGAGAGGCTCCGCGACAGCGACGCGCATGCTT 241
Db 188 GCGGAGCATGCGGAGGAGCTTGAGAGAGGCTCCGCGACAGCGACGCGCATGCTT 247
Qy 242 CCTTGAAGAGAGGCTTAAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 301
Db 248 CCTTGAAGAGAGGCTTAAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 307
Qy 302 TTGCTTCAGCGTCTCTGATGACATATCAACAGAGAGAGAGAGAGAGAGAGAGAG 361
Db 308 TTGCTTCAGCGTCTCTGATGACATATCAACAGAGAGAGAGAGAGAGAGAGAGAG 367
Qy 362 TGTGTGCGGTTCAGGAGAACCGATGACAGAGTGTGCGGTGCGACCGTATGGCATG 421
Db 368 TGTGTGCGGTTCAGGAGAACCGATGACAGAGTGTGCGGTGCGACCGTATGGCATG 427
Qy 422 TCAACAGAAAAAGTCTGCTGATGCGGAGATGGCTTGG--ACGCAACGNNATGTGC 480
Db 428 TCAACAGAAAAAGTCTGCTGATGCGGAGATGGCTTGGCCCGCAACGCAATAGTGC 487
Qy 481 CGGAGAGGGAATTTGTTGTTGAGACAGACTCGGGGAGCAATATCCCGCTGATCTCT 540
Db 488 CGGAGAGGGAATTTGTTGTTGAGACAGACTCGGGGAGCAATAT--CCCGTGAATCTCT 546

Qy 541 GCCCGGAACACTTANATACCCGCTCNCNTCANGAAGTGGCCCTCTGGATCCCTTT 600
Db 547 CCCGGAACACTTANATATTCGCCGTCATCCGAG---ANCTNCCCCTCTGGATCNCCTTT 603
Qy 601 AAACNCAANTGAAATCTCNCNTCANGAGAAGAACTCTTATGAACAGCTTTAANACNA 660
Db 604 AAACNCAANTGAAATCTCNCNTCANGAGAAGAACTCTTATGAACAGCTTTAANACNA 662
Qy 661 CGATGACNCGTCTCTCCCTCCGACATTGGCCATGGGCGCTGCTACACNCAATT 717
Db 663 NATGACNCGTCTCCACATTCACATTTGCGCAATGGGCGCTGCTCNCNCAATTTAA 722

RESULT 9
A70157
LOCUS A70157 724 bp DNA linear PAT 07-MAY-1999
DEFINITION Sequence 18 from Patent W09811228.
ACCESSION A70157
VERSION A70157.1 GI:4774572
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 724)
AUTHORS Seymour,G.B., Bird,C.R. and Medina-Suarez,R.D.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL Patent: WO 9811228-A 18 19-MAR-1998;
SETMOUR GRAHAM BARON (GB)
FEATURES
source Location/Qualifiers
1..724
/organism="unidentified"
/db_xref="taxon:32644"
/clone="U-0117"

BASE COUNT 143 a 201 c 197 g 155 t 28 others
ORIGIN
Query Match 66.5%; Score 536; DB 6; Length 724;
Best Local Similarity 89.7%; Pred. No. 1,1e-129;
Matches 617; Conservative 0; Mismatches 62; Indels 9; Gaps 5;

Qy 6 TCTCCTTCGATCAGATCTTTTGGCTGGGAACGTGAGAGGTGAGAGAGGCGGCAAT 65
Db 9 TCTCCTTCGATCAGATCTTTTGGCTGGGAACGTGAGAGGTGAGAGAGGCGGCAAT 68
Qy 66 GACGCGGCTTAAAGATGAGATTCCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 125
Db 69 GACGCGGCTTAAAGATGAGATTCCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 128
Qy 126 TTTGAACGAGAGTGGGGGTGATTGGAAGGAGAGTCTCTGCTGAGAGATGCGG 185
Db 129 TTTGAACGAGAGTGGGGGTGATTGGAAGGAGAGTCTCTGCTGAGAGATGCGG 188
Qy 186 AGCATGCGGAGAGGCTTGAGAGAGGCTCCGCGAAGCGAGAGAGAGAGAGAGAGAG 245
Db 189 AGCATGCGGAGAGGCTTGAGAGAGGCTCCGCGAAGCGAGAGAGAGAGAGAGAGAG 248
Qy 246 GGAAGAGAGGCTGTAAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 305
Db 249 GGAAGAGAGGCTGTAAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 308
Qy 306 TTGAGAGGCTCTGATGACATATCAACAGAGAGGCTGCGAGATCTTGTATCTGTC 365
Db 309 TTGAGAGGCTCTGATGACATATCAACAGAGAGGCTGCGAGATCTTGTATCTGTC 368
Qy 366 GTGGGTTCAAGCAACCGATGACAGATGCTGCGGAGAGAGAGAGAGAGAGAGAGAG 425
Db 369 GTGGGTTCAAGCAACCGATGACAGATGCTGCGGAGAGAGAGAGAGAGAGAGAGAG 428

426 CAGAAAAAGCTCGCTGACGCTGGCATTGGCTTTGGACGCAACGCMATANGTGGCCGCGA 485
|||||
429 CAGAAAAAGCTCGCTGACGCTGGCATTGGCTTTGGACGCAACGCMATANGTGGCCGCGA 488
|||||
486 CGGGGAATTTGTTGTTGTGACAGACCTCCGGGAGCAGATCCCGGTAATCTTCGCCG 545
|||||
489 CGGGG-ANTTGTGCTGTGACAGACCTCCGGGAGCAGATCCCGGTAATCTTCGCCG 547
|||||
546 GGAACACTTANATATACCCGCTCCCAANGAGTTGGCCCTCTGGGATCCCGCTTAAACN 605
|||||
548 GGAACACTTANAT-NCCTGCTCTCCCAANGAGTTGGCCCTCTGGGATCCCGCTTAAACN 603
|||||
606 CNAANTGAAATCTCNCCTCNAANGAGAACTCMTTANGAACAGC--TTTAAACNATGA 663
|||||
604 C--ACNTGANAATCCCCCNANGAGAACTCMTTANGAACAGC--TTTAAACATGAT 661
|||||
664 TGGACNCGTCTGCTCCGACATTCGC 691
|||||
662 NGACCCNGTTCACCTCCACATTCGC 689
|||||

RESULT 10

LOCUS A83000 704 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 7 from Patent WO9853085.
ACCESSION A83000
VERSION A83000.1 GI:6732480
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 704)
AUTHORS Seymour,G.B. and Bird,C.R.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL Patent: WO 9853085-A 7 26-NOV-1998;

FEATURES
SOURCE Location/Qualifiers
1..704
/organism="unclassified"
/db_xref="taxon:32644"
/clone="U-12"

BASE COUNT 146 a 190 c 191 g 149 t 28 others
ORIGIN

Query Match 63.4%; Score 510.8; DB 6; Length 704;
Best Local Similarity 86.8%; Pred. No. 4.4e-123;
Matches 603; Conservative 0; Mismatches 86; Indels 6; Gaps 5;

10 CTTCGATCACAATCTTTTGTCTGCGGAAACGTGAGAGCTGAGACGAGCGGCAATGACG 69
|||||
5 CTTCGATCACAATCTTTTGTCTGCGGAAACGTGAGAGCTGAGACGAGCGGCAATGACG 64
|||||
70 GCGGGTTAAGATGATTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 129
|||||
65 GCGGGTTAAGATGATTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 124
|||||
130 AACGAGAGCTGCGGGGTGATTTGAGAGAGAGAGCTCTGCTGAGAGATGCGGAGCA 189
|||||
125 AACGAGAGCTGCGGGGTGATTTGAGAGAGAGAGCTCTGCTGAGAGATGCGGAGCA 184
|||||
190 TCGCGAGAGAGCTTTGAGAGAGAGCTCCGCGAAGCGAGCAGCGCGATGCTTCTTGAA 249
|||||
185 TCNCGAGAGAGCTTTGAGAGAGAGCTCCGCGAAGCGAGCAGCGCGATGCTTCTTGAA 244
|||||
250 GAGAGAGCTTTAACCCTGGGAGCAGAGCGGAGCTGACGAGCAGCGGAGAGAGTTCGCG 309
|||||
245 GACAGAGCTTTNACCGAGCAGAGAGCGGAGCTTCAATGACCCGAGAGAGTTCGCG 304
|||||
310 ACGGCTCTGATGACCATTAATCAACAGAGCGGCTGCGAGATCTTTGTTATCTGCTGC 369
|||||
305 ACGGCTCTGATGACCATTAATCAACAGAGCGGCTGCGAGATCTTTGTTATCTGCTGC 364
|||||
370 GGTTCAGGCAACCCGATCGACGACTGCTGCGGCTGCGACCTGATTTGGCATGTCAACAG- 428
|||||

|||||
365 GGTTCAGGCAACCCGATCGACNACTGCTGGGGTGGCGACCCCGATGGCATGTCAACAG- 424
|||||
429 AAAAAAGCTCGCTGACCTCGGCAATTTGCTTTGGACGCAACGCMATANGTGGCCGCGAGG 488
|||||
425 AAAAAAGCTCGCTGACCTCGGCAATTTGCTTTGGACGCAACGCMATANGTGGCCGCGAGG 484
|||||
489 GGAATTTGTTGTTGTGACAGACCTCCGGGAGCAGATCCCGGTAATCTTCGCCGCGG 548
|||||
485 G-ANTTGTACNTGTGACAGACCTCCGGGAGCAGATGAT-CCCGTAATCTTCGCCGCGG 542
|||||
549 ACCTTANATAC-CCCGTCTCCCAANGAGTTGGCCCTCTGGGATCCCGCTTAAACN 607
|||||
543 ACCTTANATACNCCCGTCANCCAGAAAGT--GCCCTCTGGGATCTTCCTTAAACCC 600
|||||
608 AANTGGAATCTCNCCTCNAANGAGAACTCMTTANGAACACTTTAANATGATGGA 667
|||||
601 ACNTGANAATCTCCGCTCNAANGAGAACTCMTTANGAACACTTTTAAACAAATGCA 660
|||||
668 CNCNGTCTCTGCTCCACATTCGCAATGGCGCTG 702
|||||
661 ATGACNCCNGTTCACCTCCACATTTTGGCANTG 695
|||||

RESULT 11

LOCUS A83012 706 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 19 from Patent WO9853085.
ACCESSION A83012
VERSION A83012.1 GI:6732492
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 706)
AUTHORS Seymour,G.B. and Bird,C.R.
TITLE GENETIC CONTROL OF FRUIT RIPENING
JOURNAL Patent: WO 9853085-A 19 26-NOV-1998;

FEATURES
SOURCE Location/Qualifiers
1..706
/organism="unclassified"
/db_xref="taxon:32644"
/clone="U-114"

BASE COUNT 144 a 192 c 195 g 153 t 22 others
ORIGIN

Query Match 61.6%; Score 496.8; DB 6; Length 706;
Best Local Similarity 90.6%; Pred. No. 2.1e-119;
Matches 639; Conservative 0; Mismatches 52; Indels 14; Gaps 10;

2 GTTCTCTCTCGATCACAATCTTTTGTCTGCGGAAACGTGAGAGCTGAGACGAGCGG 61
|||||
7 GTTCTCTCTCGATCACAATCTTTTGTCTGCGGAAACGTGAGAGCTGAGAGCGG 66
|||||
62 CAATGACGCGGGTTAAGATGATTCCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 121
|||||
67 CAATGACGCGGGTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 126
|||||
122 TGGTTTGAACGAGAGCTGGGGGTGATTTGAGAGAGAGCTCTCTGCTGAGAGAT 181
|||||
127 TGGTTTGAACGAGAGCTGGGGGTGATTTGAGAGAGAGCTCTCTGCTGAGAGAT 186
|||||
182 GCGAGCATTCGCGGAGAGCTTTGAGAGAGAGCTCCGCGAAGCGGAGCGCGATGCTT 241
|||||
187 GCGAGCATTCGCGGAGAGCTTTGAGAGAGAGCTCCGCGAAGCGGAGCGCGATGCTT 246
|||||
242 CTTTGAAGAGAGGCTGTAAACCGGAGAGAGAGCGAGTGCAGAGACCCGAGAGG 301
|||||
247 CTTTGAAGAGAGGCTGTAAACAGAGAGAGAGAGCGGAGAGAGG 306
|||||
302 TTGCTTACAGGCTCTGATGACATTAATCAACAGAGCGCTGCGAGATCTTGGTATC 361
|||||

REFERENCE	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS	1 (bases 1 to 1633) Haas,B.J., Volfovsky,N., Town,C.D., Troupkhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L. Full-length messenger RNA sequences greatly improve genome annotation
TITLE	Genome Biol. (2002) In press
JOURNAL	2 (bases 1 to 1633)
REFERENCE	Brover,V., Troupkhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.
AUTHORS	Full-length cDNA from Arabidopsis thaliana Unpublished 3 (bases 1 to 1633)
TITLE	Brover,V., Troupkhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.
JOURNAL	Direct Submission Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
COMMENT	This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or later ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.
FEATURES	Location/Qualifiers 1..1633 /organism="Arabidopsis thaliana" /db_xref="taxon:3702" /clone="124816" 147..1397 /codon_start=1 /product="putative pectate lyase" /protein_id="AAK61584.1" /db_xref="GI:21537243" /translation="MAVTKLIFASALLLTLLFIGVANRSNETWHEHVAENPEVAA MVDINSINSTRERRRGFSCATGNPIDCKMDCKRWOLRRRLADSGICRNALIGER DGRVVYWDGGDDPNVPIDGETTLHAHYHDNDCKRTGAARMVTIKDELIMNSKTID GRGVNIANGACCTIOYVIRNIIIVGHVIDPKRTGAARMSSSHRGSFMADGAIL STFSSTIWDHNLSNCADSLVAVMSSTRILYSNNFTFHNNVWLHGSDNTROK VMQVTAIVNHKEGLTGMRPCRHGYHVANNDDTHDEMTAIGSAPTIINSQNREL APVNPFEKVETIGRETESESKRMKNWNMSSEDLFLNGAFITFRSGAGSNARRASLSLA KSSLVGTMTSYSGLNCRAGRRC"
CDS	BASE COUNT 434 a 375 c 344 g 480 t ORIGIN
Query Match	21.0%; Score 169.4; DB 8; Length 1633;
Best Local Similarity	63.5%; Pred. No. 1.5e-33;
Matches 304; Conservative	0; Mismatches 168; Indels 7; Gaps 4;
DB	274 GAAGCGGAGTGCAGCAGCCCGAGGAGGTTCCTTCGACGGGCCGATGACCATTAACTAAC 333 243 GAACTGTGAGTTTGAGAACCCAGATGAAGTGCCTGCATCGTAGCATGAGATTGCAAC 302 334 AGCACGGCTCCAGATCTCTGTGGTTATCTGTGCTGCGGTTGACGCAACCCGATGACGAC 393 DB 303 AGCACAGAGCGGAGAAGATAGTGGTTACTTTCCTGCGCCACCGGCAACCCATGACGAT 362 QY 394 TGCTGGCGGTGCGACCTCGATTGGCATGTCAACAAGAAAAAGCTGCTGACTGCGGCATT 453 DB 363 TGCTGGCGGTGCGACCGCAAATGTGGAGCTCGCTGCGCAACGTTTAGCCGATTGCTCATTC 422 454 GGCTTTGGAGCCAACGCNATANGGGCCGCGACGGGGAAATTTGTTTGGTTTGAAGACTC 513

Db		423	GGATTTCGCCGCAACGCATTCGGAGGGCCGGCAC - GGTCTTTTCTACTCTGTACCAGCCC	481
OY		514	CGGGGACNATGATCCCCGTGAATCCTGCCCCGGGAAACATTANATACCCGGTCNTCCAN	573
Db		482	TGGAGACGACGAT - CCGCTTAATATCCCATACCGGAAACATCCGACGCCGTGATTC ---	537
OY		574	GAAATTGCCCCCTTGCGGATTCCTCTTTAANCNCNAATGCAAAATCTCNICNANGACA	633
Db		538	- AAACGACACCACTCTGTGATCATCTTTCAAACGCAATGGTTATAAC - CTTGAAGCAAGA	595
OY		634	ACGTGTAATGACAGCTTTTAANCAATGCAATGGACNCGTGCTCTGCCAATATGGCAA	693
Db		596	CCTATCATATGACACGCTTCAAAACCATTCGATGCTGCTGATCATTTTACATCGCTTA	655
OY		694	TGGCGCCTGCTCACCAACCAATTTCTTCGCCCAANTCTTCTTCNTNGCCTCCNTCC	752
Db		656	TGGAGCTTGTCGTCGATTCATAATGCTTAGACAACTATTGTCCATGGGATTCATGCC	714
RESULT 14				
ATAC016827/c				
LOCUS	ATAC016827	90142 bp	DNA	linear PLN 24-JAN-2001
DEFINITION	Arabidopsis thaliana chromosome III BAC F17A9 genomic sequence.			
ACCESSION	complete sequence.			
VERSION	AC016827			
KEYWORDS	AC016827.7	GI:12408743		
SOURCE	HTC.			
ORGANISM	Arabidopsis thaliana.			
REFERENCE	Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
AUTHORS	Lin,X., Kaul,S., Town,C.D., Beutlo,M.-I., Creasy,T.H., Haas,B., Wu,D., Rongning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Barneshead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.			
JOURNAL	Arabidopsis thaliana chromosome III BAC F17A9 genomic sequence Unpublished			
TITLE	2 (bases 1 to 90142)			
REFERENCE	Lin,X. and Kaul,S.			
AUTHORS	Direct Submission			
JOURNAL	Submitted (08-DEC-1999) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, xlinetlgr.org			
REFERENCE	3 (bases 1 to 90142)			
AUTHORS	Lin,X.			
JOURNAL	Direct Submission			
REFERENCE	Submitted (24-JAN-2001) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA			
AUTHORS	On Jan 21, 2001 this sequence version replaced gi:12280775.			
JOURNAL	Address all correspondence to:tatletlgr.org			
COMMENT				

BAC clone:F17A9 is from Arabidopsis chromosome III and is near the molecular marker m1357.
The orientation of the sequence is from SP6 to T7 end of the BAC clone.

Genes were identified by a combination of three methods: Gene prediction programs including GRILL (available by anonymous ftp from arthur.epm.ornl.gov), Genefinder (Phil Green, University of Washington), GENSCAN (Chris Burge, <http://genomic.stanford.edu/~chris/GENSCANW.html>), and NetPlantGene (<http://www.cbs.dtu.dk/netpgene/cbsnetpgene.html>), searches of the complete sequence against a peptide database and the Arabidopsis EST database at tigr (<http://www.tigr.org/cdb/at/est.html>). Annotated genes are named to indicate the level of evidence for their annotation. Genes w/ith similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are

identified by RepeatMasker (Arlan Smit,
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GenCore version 5.1.6
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Run on: June 23, 2003, 22:19:35 ; Search time 252 Seconds
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Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	543.8	67.5	727	19	AAV28658
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9	496.8	61.6	706	20	AAV69458

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13	144.4	17.9	749	20	AAV69445	Banana fruit ripen
14	142.8	17.7	842	19	AAV28659	Ripening banana pu
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34	114.6	14.2	1514	21	AAV41563	Arabidopsis thalia
35	113	14.0	1615	21	AAV51025	Arabidopsis thalia
36	113	14.0	1617	21	AAV41994	Arabidopsis thalia
37	110.4	13.7	1221	21	AAV47293	Arabidopsis thalia
38	110.4	13.7	1631	21	AAV33659	Arabidopsis thalia
39	110.4	13.7	1631	21	AAV49928	Arabidopsis thalia
40	109.6	13.6	1125	21	AAV42903	Arabidopsis thalia
41	94	11.7	438	21	AAV31518	Plant microsatellit
42	93.4	11.6	460	24	AAV93674	Arabidopsis thalia
43	83.4	10.3	1807	21	AAV51305	Arabidopsis thalia
44	83.4	10.3	1812	21	AAV39116	Arabidopsis thalia
45	81.8	10.1	1523	21	AAV31573	Arabidopsis thalia

ALIGNMENTS

RESULT 1	
AAV28655	AAV28655 standard; CDNA; 806 BP.
XX	XX
AC	AAV28655;
XX	XX
DT	29-JUL-1998 (first entry)
XX	XX
DE	Ripening banana pulp cDNA clone U-068 SEQ ID NO:13.
XX	XX
KW	Banana; ripening; pulp; Musa acuminata cv. Grand Nain; fruit;
KM	genetic control; tissue senescence; ss.
XX	XX
OS	Musa acuminata.
XX	XX
PN	W09811228-A2.
XX	XX
PD	19-MAR-1998.
XX	XX
PE	08-SEP-1997; 97WO-GB02424.
XX	XX
PR	25-APR-1997; 97GB-0008366.
XX	XX
PR	10-SEP-1996; 96GB-0018862.
XX	XX
PA	(ZENE) ZENCA LTD.
XX	XX
PI	Bird CR, Medina-Suarez RDJ, Seymour GB;
XX	XX
DR	WPL; 1998-207389/18.
XX	XX
PT	Modulation of ripening or tissue senescence in bananas - comprises use of DNA isolated from ripening banana pulp to produce genetically

PT modified fruit

XX Claim 1; Page 26; 72pp; English.

CC The present sequence represents a cDNA clone isolated from ripening
CC banana pulp. 57 clones were isolated and are given in AAV28643 to
CC AAV28659. The cDNA clone sequences can be used in a method of modulating
CC ripening or tissue senescence processes in plants of the genus Musa. The
CC method comprises: (a) inserting into the plant material at least 1 of the
CC 57 sequences (as above); (b) regenerating the plant material, and (c)
CC selecting from the transformed regenerants, plants with modulated
CC ripening or tissue senescence characteristics. Also described in the
CC present invention are: (1) plants, their progeny, seed and material
CC obtained from the plants, produced by the above method; (2) a vector
CC functional in plants comprising a promoter region which is operably in
CC plant cells, a polynucleotide sequence as defined above, and a
CC transcription termination sequence; and (3) a method of controlling
CC plant pathogens comprising the application of anti-pathogenic agent to
CC plants of (1).

XX Sequence 806 BP; 157 A; 229 C; 212 G; 180 T; 28 other;

Query Match 96.5%; Score 778; DB 19; Length 806;

Best Local Similarity 100.0%; Pred. No. 1e-221;
Matches 806; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TGTCTCTCTCTGATCATCTTTTGTCTCTGGAACGTGAGAGTGAGACGAGGCG 60
1 TGTCTCTCTCTGATCATCTTTTGTCTCTGGAACGTGAGAGTGAGACGAGGCG 60
61 GCAATGAGAGGCGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCT 120
61 GCAATGAGAGGCGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCT 120
121 CTGCTTTGAACGAGAGTGCGGGGTGAGATTTGGAACGAGAGTCTCTGCGTGGAGAT 180
121 CTGCTTTGAACGAGAGTGCGGGGTGAGATTTGGAACGAGAGTCTCTGCGTGGAGAT 180
181 GCGGAGAGATCGCGGAGAGCTTGGAGAGAGCGCTCGCGAAGCGAGCGCGCGATCT 240
181 GCGGAGAGATCGCGGAGAGCTTGGAGAGAGCGCTCGCGAAGCGAGCGCGCGATCT 240
241 GCGGAGAGATCGCGGAGAGCTTGGAGAGAGCGCTCGCGAAGCGAGCGCGCGATCT 240
241 GCGGAGAGATCGCGGAGAGCTTGGAGAGAGCGCTCGCGAAGCGAGCGCGCGATCT 240
241 TCCCTTGAAGAGAGGCTGTAAACCGGGGAGAGAAAGCGCGAGTGAAGAGAGAGAG 300
241 TCCCTTGAAGAGAGGCTGTAAACCGGGGAGAGAAAGCGCGAGTGAAGAGAGAGAG 300
241 TCCCTTGAAGAGAGGCTGTAAACCGGGGAGAGAAAGCGCGAGTGAAGAGAGAGAG 300
241 TCCCTTGAAGAGAGGCTGTAAACCGGGGAGAGAAAGCGCGAGTGAAGAGAGAGAG 300
301 GTTGTCTGAGAGGCTGTATGACATTAATCAACAGACGAGCGTGGAGATCTTGTAT 360
301 GTTGTCTGAGAGGCTGTATGACATTAATCAACAGACGAGCGTGGAGATCTTGTAT 360
361 CTGCTGAGAGGCTGTATGACATTAATCAACAGACGAGCGTGGAGATCTTGTAT 420
361 CTGCTGAGAGGCTGTATGACATTAATCAACAGACGAGCGTGGAGATCTTGTAT 420
421 GTTGTCTGAGAGGCTGTATGACATTAATCAACAGACGAGCGTGGAGATCTTGTAT 480
421 GTTGTCTGAGAGGCTGTATGACATTAATCAACAGACGAGCGTGGAGATCTTGTAT 480
421 GTTGTCTGAGAGGCTGTATGACATTAATCAACAGACGAGCGTGGAGATCTTGTAT 480
421 GTTGTCTGAGAGGCTGTATGACATTAATCAACAGACGAGCGTGGAGATCTTGTAT 480
481 GCGGAGAGGCTGTATGACATTAATCAACAGACGAGCGTGGAGATCTTGTAT 540
481 GCGGAGAGGCTGTATGACATTAATCAACAGACGAGCGTGGAGATCTTGTAT 540
541 GCGGAGAGGCTGTATGACATTAATCAACAGACGAGCGTGGAGATCTTGTAT 600
541 GCGGAGAGGCTGTATGACATTAATCAACAGACGAGCGTGGAGATCTTGTAT 600
601 AAACNCAANTGAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
601 AAACNCAANTGAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
661 CGATGAGAGGCTGTATGACATTAATCAACAGACGAGCGTGGAGATCTTGTAT 720
661 CGATGAGAGGCTGTATGACATTAATCAACAGACGAGCGTGGAGATCTTGTAT 720
720 CGATGAGAGGCTGTATGACATTAATCAACAGACGAGCGTGGAGATCTTGTAT 720

721 TCCCAACNTCT 780
721 TCCCAACNTCT 780
781 CCCNCTCCCT 806
781 CCCNCTCCCT 806

RESULT 2

AAV69457
ID AAV69457 standard; cDNA; 748 BP.

AAV69457;

15-MAR-1999 (first entry)

Banana fruit ripening-related clone U-113 cDNA.

Fruit ripening; banana; modulator; tissue senescence; crop; plant;

triploid; plant breeding; ss.

Musa acuminata.

W09853085-A1.

26-NOV-1998.

05-MAY-1998; 98WO-GB01297.

20-MAY-1997; 97GB-0010370.

(ZENEC) ZENEC LTD.

Bird CR, Medina-Suarez RDJ, Seymour GB.

WPI: 1999-059745/05.

New method of modulating fruit ripening or tissue senescence

characteristics of Musa plants - by introducing DNA sequences,

useful in processes for modifying plant/fruit ripening

characteristics

Claim 1; Page 29; 78pp; English.

AAV69440-69512 are cDNA sequences which are used in a method to
modulate the fruit ripening or tissue senescence characteristics of Musa
acuminata (banana) plants. The method provides a recombinant way of
modulating ripening/senescence characteristics of bananas, which are a
globally important crop. In particular, the method can modulate such
characteristics in the desert banana, which due to its triploid nature
is unaffected by conventional plant breeding techniques.

Sequence 748 BP; 154 A; 211 C; 206 G; 163 T; 14 other;

Query Match 73.4%; Score 591.8; DB 20; Length 748;

Best Local Similarity 91.7%; Pred. No. 3.4e-166;
Matches 664; Conservative 0; Mismatches 52; Indels 8; Gaps 4;

1 TGTCTCTCTCTGATCATCTTTTGTCTCTGGAACGTGAGAGTGAGACGAGGCG 60
1 TGTCTCTCTCTGATCATCTTTTGTCTCTGGAACGTGAGAGTGAGACGAGGCG 60
16 TGTCTCTCTCTGATCATCTTTTGTCTCTGGAACGTGAGAGTGAGACGAGGCG 75
61 GCATGAGAGGCGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
61 GCATGAGAGGCGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
76 GCATGAGAGGCGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 135
76 GCATGAGAGGCGGTTTAAGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 135
121 CTGCTTTGAACGAGAGTGCGGGGTGAGATTTGGAACGAGAGTCTCTGCGTGGAGAT 180
121 CTGCTTTGAACGAGAGTGCGGGGTGAGATTTGGAACGAGAGTCTCTGCGTGGAGAT 180
136 CTGCTTTGAACGAGAGTGCGGGGTGAGATTTGGAACGAGAGTCTCTGCGTGGAGAT 195
136 CTGCTTTGAACGAGAGTGCGGGGTGAGATTTGGAACGAGAGTCTCTGCGTGGAGAT 195
181 GCGGAGAGATCGCGGAGAGCTTGAAGAGAGCGCTCGCGAAGCGAGCGAGCGGATGCT 240

Dd		196	GCGGAGCATCGGGAGGCTTGAGAGAGGCCCTCCGCACGCGCAGCCGCGATGCT	255
Oy		241	TCTTGTGAAGAAGGGCTTAACCCCCGGGAGAGAAAGCCGCACTGCAGCACCCCAGAGAG	300
Dd		256	TCTTTGAAGAGAGGGCTGTAAACCAGGGGAGAGAAAGCCGCACTGCAGCACCCCAGAGAG	315
Oy		301	GTTCGTTGCAGCGTCTGATGACAATAATCAACAGACGCGTCCGAGATCTCTTGGTTAT	360
Dd		316	GTTGGTTGAGCGTCTCTGACGACATTAATCAACAGACGCGTCCGAGATCTCTTGGTTAT	375
Oy		361	CTGTGTCGGGTTTCAGGCAACCCGATCGACACTGTGGCGGTGCGACCCCTGATTGGCAT	420
Dd		376	CTGTGTCGGGTTTCAGGCAACCCGATCGACACTGTGGCGGTGCGACCCCTGATTGGCAT	435
Oy		421	GTCAAACAAAAAAGCTCGCTGACATGCGGCACTTAGGCTTGGAGCGCAACGMATANGTGGC	480
Dd		436	GTCAAACAAAAAAGCTCGCTGACATGCGGCACTTAGGCTTGGAGCGCAACGMATANGTGGC	495
Oy		481	CGCCAGCGGGGATTTTGTTGGTTGTACACAGACTCCGGGGGCMANATGATCCCCGTGAATCTTC	540
Dd		496	CGCCAGCGGGGANTTTGATGCTGTGTGACAGACTCCGGGGGCMANATGATCCCCGTGAATCTTC	555
Oy		541	GCCCGGGGAACTTANATACC CGCGTNCNTCCANGAAGTTGCCCCCTCTGGGATCCCTTT	600
Dd		556	CCCCGGGAACTTANATACC CGCGTNCNTCCANGAAGTTGCCCCCTCTGGGATCCCTTT	610
Oy		601	A AACNMANATNGAATATCTCNCTCANANGGAAGACTCNTTATGACAGCTTTAANA CNAT	660
Dd		611	A AACNMANATNGAATATCTCNCTCANANGGAAGACTCNTTATGACAGCTTTAANA CNAT	669
Oy		661	CGATGACNCNGTGTCTGTCCATTCGCAATTGGCGCCTGCTCNCACCAATTTCCN	720
Dd		670	CGATGACNCNGTGTCTGTCCATTCGCAATTGGCGCCTGCTCNCACCAATTTCCN	727
Oy		721	TC CC 724	
Dd		728	CACC 731	
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RESULT 3				
ID	AAV69450			
XX	AAV69450 standard; cDNA; 745 BP.			
AC	AAV69450;			
DT	15-MAR-1999 (first entry)			
DE	Banana fruit ripening-related clone U-52 cDNA.			
KW	Fruit ripening; banana; modulator; tissue senescence; crop; plant;			
OS	Musa acuminata.			
PJ	WO9853085-A1.			
PD	26-NOV-1998.			
PE	05-MAY-1998; 98MO-GB01297.			
PR	20-MAY-1997; 97GB-0010370.			
PA	(ZENEC) ZENECA LTD.			
P1	Bird CR, Medina-Suarez RDJ, Seymour GB;			
DR	WPI; 1999-059745/05.			
PT	New method of modulating fruit ripening or tissue senescence			
PT	characteristics of Musa plants - by introducing DNA sequences,			
PT	useful in processes for modifying plant/fruit ripening			
PT	characteristics			

XX Claim 1; Page 24-25; 78pp; English.

PS

CC AAY69440-v69512 are cDNA sequences which are used in a method to

CC modulate the fruit ripening or tissue senescence characteristics of Musa

CC acuminata (bananas) plants. The method provides a recombinant way of

CC modulating ripening/senescence characteristics of bananas, which are a

CC globally important crop. In particular, the method can modulate such

CC characteristics in the dessert banana, which due to its triploid nature

CC is unaffected by conventional plant breeding techniques.

XX

Sequence 745 BP; 153 A; 204 C; 203 G; 163 T; 22 other;

XX

Query Match	73.3%	Score 591.2;	DB 20;	Length 745;
Best Local Similarity	90.5%;	Pred. No. 5.2e-166;		
Matches 673;	Conservative 0;	Mismatches 61;	Indels 10;	Gaps 5
QY 1	TGTTCTCCCTTCGATC	ATCTTTTGGCTCTGGGAAACGTGAGAGTGAGACGAGGCG	60	
DB 7	TGTTCTCCCTTCGATC	ATCTTTTGGCTCTGGGAAACGTGAGAGTGAGACGAGGCG	66	
QY 61	GCATAGACGGGGGGTTAA	AGATTCCTCTCTGCTTCTTCTTGGGCTTCTG	120	
DB 67	GCATAGACGGGGGGTTAA	AGATTCCTCTCTGCTTCTTCTTGGGCTTCTG	126	
QY 121	CTGTTTTGAACGAGAGT	CGGGGGGAGATTGGAAACGAGAGTCTTGCGCTCGAGGAT	180	
DB 127	CTGTTTTGAACGAGAGT	CGGGGGGAGATTGGAAACGAGAGTCTTGCGCTCGAGGAT	186	
QY 181	GGCGGAGCATGCCGAG	GAGCTTGAGAGAGCTCTCGGAAACGAGACGAGCGCGGATGCT	240	
DB 187	GGCGGAGCATGCCGAG	GAGCTTGAGAGAGCTCTCGGAAACGAGACGAGCGCGGATGCT	246	
QY 241	TCCTTGAAGAGAGGGCT	GTAAACCGGGGAGAGAAAGCCGAGTGAAGACCCCGAGGAG	300	
DB 247	TCCTTGAAGAGAGGGCT	GTAAACCGGGGAGAGAAAGCCGAGTGAAGACCCCGAGGAG	306	
QY 301	GTTGCTTGACGGGTCT	GATGACCAATTAACAACAGACGAGCTCGAGATCTCTTGGTTAT	360	
DB 307	GTTGCTTGACGGGTCT	GATGACCAATTAACAACAGACGAGCTCGAGATCTCTTGGTTAT	366	
QY 361	CTGTCGTGCGGTTGAG	GAACCCGATGACGAGCTGTGGGCGTGGGACCTCGATGGCAT	420	
DB 367	CTGTCGTGCGGTTGAG	GAACCCGATGACGAGCTGTGGGCGTGGGACCTCGATGGCAT	426	
QY 421	GTCAACAG-AAAAAAG	CTGCTGATGGGCAATGGCTTTGGACCAACGCAATANGTGG	479	
DB 427	GTCAACAGAAAAAAG	CTGCTGATGGGCAATGGCTTTGGACCAACGCAATANGTGG	486	
QY 480	CCGGAGACGGGGAAT	TGTTGCTGTGACAGACTCCGGGACNATATCCCGTGATCT	539	
DB 487	CCGGAGACGGG-ANT	TGTACGTGTGAGAGACTCCGGGACNATAT-CCGCTGATCT	544	
QY 540	CGCCCGGAAACCTA	NATACCCGCTCMTCANAAAGTTGGCCCCCTGGGATCCCGCT	599	
DB 545	CNCCCGGAAACCTA	NATACCCGCTCMTCANAAAGTTGGCCCCCTGGGATCCCGCT	600	
QY 600	TAAACNCAANTGAA	ATCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT	656	
DB 601	TAAACNCAANTGAA	ATCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT	660	
QY 657	CNATGATGAGACNG	TGCTCTGCTGACATTTGCCAATGCGGCTGCTGACACNCAAT	716	
DB 661	ACATGATGAGACCG	TGTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT	720	
QY 717	TTCNTCCCAACNT	CTCTCTCCT 740		
DB 721	TACATCACCAAG	TATCTCTCAT 744		

RESULT 4

AAV69447

AAV69447 standard; cDNA; 793 BP.


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XX AAV69447;
AC 15-MAR-1999 (first entry)
XX
DE Banana fruit ripening-related clone U-22 cDNA.
XX
KM Fruit ripening; banana; modulator; tissue senescence; crop; plant;
XX triploid; plant breeding; ss.
XX
OS Musa acuminata.
XX
PN WO9853085-A1.
XX
PD 26-NOV-1998.
XX
PF 05-MAY-1998; 98WO-GB01297.
XX
PR 20-MAY-1997; 97GB-0010370.
XX
PA (ZENB ) ZENECA LTD.
XX
PI Bird CR, Medina-Suarez RDJ, Seymour GB;
XX
DR WPI; 1999-059745/05.
XX
PT New method of modulating fruit ripening or tissue senescence
PT characteristics of Musa plants - by introducing DNA sequences,
PT useful in processes for modifying plant/fruit ripening
PT characteristics
XX
PS Claim 1; Page 22-23; 78pp; English.
XX
CC AAV69440-V69512 are cDNA sequences which are used in a method to
CC modulate the fruit ripening or tissue senescence characteristics of Musa
CC acuminata (banana) plants. The method provides a recombinant way of
CC modulating ripening/senescence characteristics of bananas, which are a
CC globally important crop. In particular, the method can modulate such
CC characteristics in the desert banana, which due to its triploid nature
CC is unaffected by conventional plant breeding techniques.
XX
SQ Sequence 793 BP; 170 A; 222 C; 215 G; 171 T; 15 other;

Query Match 73.1%; Score 588.8; DB 20; Length 793;
Best Local Similarity 88.7%; Pred. No. 2.8e-165;
Matches 705; Conservative 0; Mismatches 77; Indels 13; Gaps 7;

OY 1 TGTCTCTCTCGATGACATCTTTTGTCTGGGAACGTGAGAGTGAGAGGGCG 60
DB 8 TGTCTCTCTCTCGATGACATCTTTTGTCTGGGAACGTGAGAGTGAGAGGGCG 67
OY 61 GCATGACGGCGGTTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 68 GCATGACGGCGGTTTAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 127
OY 121 CTGCTTTTGAAGAGGAGTCTGGGGTGATGGAACGAGAGTCTCTCTCTCTCT 180
DB 128 CTGCTTTTGAAGAGGAGTCTGGGGTGATGGAACGAGAGTCTCTCTCTCTCT 187
OY 181 GCGGAGCATCGCGAGAGAGCTTTGAGAGAGGCTCCGGAACGAGAGCGCCGATGCT 240
DB 188 GCGGAGCATCGCGAGAGAGCTTTGAGAGAGGCTCCGGAACGAGAGCGCCGATGCT 247
OY 241 TCTTTGAGAGAGGAGTCTGTAACCGGAGCAGAGAGCGAGTGCAGAGACCCGAGAG 300
DB 248 TCTTTGAGAGAGGAGTCTGTAACCGGAGCAGAGAGCGAGTGCAGAGACCCGAGAG 307
OY 301 GTTGCTTGAGAGGAGTCTGTAACCGAGATCAACACAGAGCGCTCCGAGATCTTTGCTAT 360
DB 308 GTTGCTTGAGAGGAGTCTGTAACCGAGATCAACACAGAGCGCTCCGAGATCTTTGCTAT 367
OY 361 CTGCTGTCGGTTCAGGACCGGATGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420

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DB 368 CTGCTGTCGGTTCAGGACCGGATGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 427
OY 421 GTCAACAG-AAAAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479
DB 428 GTCAACAGAAAAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 487
OY 480 CCGCGAGCGGGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 539
DB 488 CCGCGAGCGGGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
OY 540 CCGCGAGCGGGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 599
DB 547 GCGCGAGCGGGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
OY 600 TAAACNCAANTGAAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 659
DB 603 TAAACNCAANTGAAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
OY 660 TCGATGAGACNCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719
DB 661 TCGATGAGACNCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
OY 720 NTCCCAACNCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777
DB 718 ATCCCAACNCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777
OY 778 NTCCCAACNCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792
DB 778 NTCCCAACNCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 792

RESULT 5
AAV69460
ID AAV69460 standard; cDNA; 727 BP.
XX
AC AAV69460;
XX
DE 15-MAR-1999 (first entry)
XX
DE Banana fruit ripening-related clone U-139 cDNA.
XX
KM Fruit ripening; banana; modulator; tissue senescence; crop; plant;
XX triploid; plant breeding; ss.
XX
OS Musa acuminata.
XX
PN WO9853085-A1.
XX
PD 26-NOV-1998.
XX
PF 05-MAY-1998; 98WO-GB01297.
XX
PR 20-MAY-1997; 97GB-0010370.
XX
PA (ZENB ) ZENECA LTD.
XX
PI Bird CR, Medina-Suarez RDJ, Seymour GB;
XX
DR WPI; 1999-059745/05.
XX
PT New method of modulating fruit ripening or tissue senescence
PT characteristics of Musa plants - by introducing DNA sequences,
PT useful in processes for modifying plant/fruit ripening
PT characteristics
XX
PS Claim 1; Page 30-31; 78pp; English.
XX
CC AAV69440-V69512 are cDNA sequences which are used in a method to
CC modulate the fruit ripening or tissue senescence characteristics of Musa
CC acuminata (banana) plants. The method provides a recombinant way of
CC modulating ripening/senescence characteristics of bananas, which are a
CC globally important crop. In particular, the method can modulate such
CC characteristics in the desert banana, which due to its triploid nature

```

CC is unaffected by conventional plant breeding techniques.

XX Sequence 727 BP; 144 A; 199 C; 202 G; 157 T; 25 other;

Query Match 71.0%; Score 572.2; DB 20; Length 727;

Best Local Similarity 90.9%; Pred. No. 2.4e-160;

Matches 653; Conservative 0; Mismatches 57; Indels 8; Gaps 5;

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QY 1 TGGTCTGCTTCATCATCTTTTGTCTGGGAAACGTGAGAGTGAACGAGGCG 60
DB 16 TGTCTCTCTTCATCATCTTTTGTCTGGGAAACGTGAGAGTGAACGAGGCG 75
QY 61 GCAATGACGGCGGCTTAAATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCT 120
DB 76 GCAATGACGGCGGCTTAAATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCT 135
QY 121 CTGGTTTGAACGAGGCTGGGGGATGATGGAAGCGAGAGTCTCTGCTGAGAT 180
DB 136 CTGGTTTGAACGAGGCTGGGGGATGATGGAAGCGAGAGTCTCTGCTGAGAT 195
QY 181 GCGGAGCATGCGGAGAGGCTTGAAGAGGCTCCGGAACGGAGCGCGATGCT 240
DB 196 GCGGAGCATGCGGAGAGGCTTGAAGAGGCTCCGGAACGGAGCGCGATGCT 255
QY 241 TCTTTGAAAGAGGCTGTAAACCGGCGAGAGAGCGGAGTGGAGCGCGAGAG 300
DB 256 TCTTTGAAAGAGGCTGTAAACCGGCGAGAGAGCGGAGTGGAGCGCGAGAG 315
QY 301 GTTCTCTGACGGCTCTGATGATCAATTAACAGCAGGCTGGAGATCTTGGTAT 360
DB 316 GTTCTCTGACGGCTCTGATGATCAATTAACAGCAGGCTGGAGATCTTGGTAT 375
QY 361 CTGTCTGCGGCTTGAAGAGGCTTGAAGAGGCTTGAAGAGGCTTGAAGAGG 419
DB 376 CTGTCTGCGGCTTGAAGAGGCTTGAAGAGGCTTGAAGAGGCTTGAAGAGG 435
QY 420 TGTCAACAGAAAAAGCTCGCTGACTGGGCTTGGCTTGGAGCAACGCTATG 479
DB 436 TGTCAACAGAAAAAGCTCGCTGACTGGGCTTGGCTTGGAGCAACGCTATG 495
QY 480 CCGGAGCGGAGATTTGCTGCTGAGACAGCTCCGGGAGCATGCTCCGCTGAT 539
DB 496 CCGGAGCGGAGATTTGCTGCTGAGACAGCTCCGGGAGCATGCTCCGCTGAT 554
QY 540 CCGGAGCGGAGATTTGCTGCTGAGACAGCTCCGGGAGCATGCTCCGCTGAT 599
DB 555 CCGGAGCGGAGATTTGCTGCTGAGACAGCTCCGGGAGCATGCTCCGCTGAT 610
QY 600 TAAACNCAATGGAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 659
DB 611 TAAACNCAATGGAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 669
QY 660 TCGATGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 717
DB 670 TCGATGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 726

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RESULT 6
AAV28658
ID AAV28658 standard; cDNA: 727 BP.

XX AAV28658;

XX 29-JUL-1998 (first entry)

DE Ripening banana pulp cDNA clone U-089 seq ID NO:16.

XX Banana; ripening; pulp; Musa acuminata cv. Grand Nain; fruit;

XX genetic control; tissue senescence; ss.

XX Musa acuminata.

XX OS
XX PN W0811228-A2.

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XX 19-MAR-1998.
PD 08-SEP-1997; 97MO-GB02424.
XX 25-APR-1997; 97GB-0008366.
PR 10-SEP-1996; 96GB-0018862.
XX (ZENEC) ZENEC LTD.
XX Bird CR, Medina-Suarez RDI, Seymour GB.
DR WPI: 1998-207389/18.
XX Modulation of ripening or tissue senescence in bananas - comprises
PR use of DNA isolated from ripening banana pulp to produce genetically
PT modified fruit
XX Claim 1: Page 28; 72pp; English.
XX
XX The present sequence represents a cDNA clone isolated from ripening
CC banana pulp. 57 clones were isolated and are given in AAV28643 to
CC AAV28699. The cDNA clone sequences can be used in a method of modulating
CC ripening or tissue senescence process in plants of the genus Musa. The
CC method comprises: (a) inserting into the plant material at least 1 of the
CC 57 sequences (as above); (b) regenerating the plant material, and (c)
CC selecting from the transformed regenerants, plants with modulated
CC ripening or tissue senescence characteristics. Also described in the
CC present invention are: (1) plants, their progeny, seed and material
CC obtained from the plants, produced by the above method; (2) a vector
CC functional in plants comprising a promoter region which is operably in
CC plant cells, a polynucleotide sequence as defined above, and a
CC transcription termination sequence; and (3) a method of controlling
CC plant pathogens comprising the application of anti-pathogenic agent to
CC plants of (1).
XX
SQ Sequence 727 BP; 145 A; 205 C; 196 G; 159 T; 22 other;

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Query Match 67.5%; Score 543.8; DB 19; Length 727;
Best Local Similarity 86.6%; Pred. No. 7e-152;
Matches 628; Conservative 0; Mismatches 91; Indels 6; Gaps 4;

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QY 2 GTTCTCTCTGATCATCTTTTGTCTGGGAAACGTGAGAGTGAACGAGGCGG 61
DB 8 GTTCTCTCTGATCATCTTTTGTCTGGGAAACGTGAGAGTGAACGAGGCGG 67
QY 62 CAATGAGCGGCGTTAATGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 121
DB 68 CAATGAGCGGCGTTAATGATGATTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 127
QY 122 TGTGTTTGAACGAGAGTGGGGGATGATGGAAGGAGGCTCTGCTGAGAGATG 181
DB 128 TGTGTTTGAACGAGAGTGGGGGATGATGGAAGGAGGCTCTGCTGAGAGATG 187
QY 182 GCGGAGCATGCGGAGAGGCTTGAAGAGGCTCCGGAACGCGACGCGCGATGCTT 241
DB 188 GCGGAGCATGCGGAGAGGCTTGAAGAGGCTCCGGAACGCGACGCGCGATGCTT 247
QY 242 CTTTGAAGAGAGGCTGTAACCCGCGAGAGAGAGCGAGTGGAGACCCCGAGGAGG 301
DB 248 CTTTGAAGAGAGGCTGTAACCCGCGAGAGAGAGCGAGTGGAGACCCCGAGGAGG 307
QY 302 TTGCTTGAAGAGGCTGTAACCAATTAACAGAGCGCTGCGAGATCTTGGTATTC 361
DB 308 TTGCTTGAAGAGGCTGTAACCAATTAACAGAGCGCTGCGAGATCTTGGTATTC 367
QY 362 TGTGTTGCTTGAAGAGCAACCGGATGAGAGCTGCTGCGGCTGCGAGATGAGCATG 421
DB 368 TGTGTTGCTTGAAGAGCAACCGGATGAGAGCTGCTGCGGCTGCGAGATGAGCATG 427
QY 422 TCAACAGAAAAAGCTGCTGAGTGGGCTTGGCTTGG-ACGCAACGCTATGNGTGGC 480
DB 428 TCAACAGAAAAAGCTGCTGAGTGGGCTTGGCTTGG-ACGCAACGCTATGNGTGGC 487

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PD 26-NOV-1998.
 XX 05-MAY-1998; 98WO-GB01297.
 XX 20-MAY-1997; 97GB-0010370.
 XX (ZENEC) ZENEC LTD.
 PA Bird CR, Medina-Suarez RDJ, Seymour GB;
 XX WPI: 1999-059745/05.
 DR
 XX
 PT New method of modulating fruit ripening or tissue senescence
 PT characteristics of Musa plants - by introducing DNA sequences,
 PT useful in processes for modifying plant/fruit ripening
 PT characteristics
 XX
 PS Claim 1; Page 22; 78pp; English.
 CC AAV69440-V69512 are cDNA sequences which are used in a method to
 CC modulate the fruit ripening or tissue senescence characteristics of Musa
 CC acuminata (banana) plants. The method provides a recombinant way of
 CC modulating ripening/senescence characteristics of bananas, which are a
 CC globally important crop. In particular, the method can modulate such
 CC characteristics in the desert banana, which due to its triploid nature
 CC is unaffected by conventional plant breeding techniques.
 CC
 XX
 S0 Sequence 704 BP; 146 A; 190 C; 191 G; 149 T; 28 other;
 Query Match 63.4%; Score 510.8; DB 20; Length 704;
 Best Local Similarity 86.8%; Pred. No. 4.8e-142;
 Matches 603; Conservative 0; Mismatches 86; Indels 6; Gaps 5;
 QY 10 CTTCGATCAGATCTTTTGTCTCTGGAAACGTGAGAGTGAGAGAGGCGGCAATGACG 69
 DB 5 CTTCGATCAGATCTTTTGTCTCTGGAAACGTGAGAGTGAGAGAGGCGGCAATGACG 64
 QY 70 GCGGGTTTAAAGATGATCT 129
 DB 65 GCGGGTTTAAAGATGATCT 124
 QY 130 AAGGAGGTGCGGGGGTGGATGGAAGGAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 189
 DB 125 AAGGAGGTGCGGGGGTGGATGGAAGGAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 184
 QY 190 TCGCGAGAGAGCTTGAAGAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 249
 DB 185 TCGCGAGAGAGCTTGAAGAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 244
 QY 250 GAGAGGCTGTAAACCGGGGAGAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 309
 DB 245 GAGAGGCTGTAAACCGGGGAGAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 304
 QY 310 ACGGTCCTGATGACATATCAACAGAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 369
 DB 305 ACGGTCCTGATGACATATCAACAGAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 364
 QY 370 GTTCGAGGCAACCGATGAGAGCTGTGGGCTGAGAGCTGTGATGATGATGATGATGATGATGAT 428
 DB 365 GTTCGAGGCAACCGATGAGAGCTGTGGGCTGAGAGCTGTGATGATGATGATGATGATGATGAT 424
 QY 429 AAAAAAGCTGCTGAGTGGCGGATGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 488
 DB 425 AAAAAAGCTGCTGAGTGGCGGATGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 484
 QY 489 GGAATTTCTGCTGTGAGAGAGCTGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 548
 DB 485 GG-AMTGTACNTTGTACAGAGCTGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 542
 QY 549 ACACTTANATAG-CCGCT 607
 DB 543 ACACTTANATAG-CCGCT 600

QY 608 AANTGGAATCT 667
 DB 601 ACNTGGAATCT 660
 QY 668 CACGATGCT 702
 DB 661 ATGAGACNCGTGTCT 695
 RESULT 9
 ID AAV69458 standard; cDNA; 706 BP.
 XX AAV69458;
 AC AAV69458;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Banana fruit ripening-related clone U-114 cDNA.
 XX
 KW Fruit ripening; banana; modulator; tissue senescence; crop; plant;
 KW triploid; plant breeding; ss.
 OS Musa acuminata.
 PN W09853085-A1.
 XX
 PD 26-NOV-1998.
 PE 05-MAY-1998; 98WO-GB01297.
 XX
 PR 20-MAY-1997; 97GB-0010370.
 XX
 PA (ZENEC) ZENEC LTD.
 PT Bird CR, Medina-Suarez RDJ, Seymour GB;
 XX WPI: 1999-059745/05.
 DR
 XX
 PT New method of modulating fruit ripening or tissue senescence
 PT characteristics of Musa plants - by introducing DNA sequences,
 PT useful in processes for modifying plant/fruit ripening
 PT characteristics
 XX
 PS Claim 1; Page 29-30; 78pp; English.
 CC AAV69440-V69512 are cDNA sequences which are used in a method to
 CC modulate the fruit ripening or tissue senescence characteristics of Musa
 CC acuminata (banana) plants. The method provides a recombinant way of
 CC modulating ripening/senescence characteristics of bananas, which are a
 CC globally important crop. In particular, the method can modulate such
 CC characteristics in the desert banana, which due to its triploid nature
 CC is unaffected by conventional plant breeding techniques.
 CC
 XX
 S0 Sequence 706 BP; 144 A; 192 C; 195 G; 153 T; 22 other;
 Query Match 61.6%; Score 496.8; DB 20; Length 706;
 Best Local Similarity 90.6%; Pred. No. 7.2e-138;
 Matches 639; Conservative 0; Mismatches 52; Indels 14; Gaps 10;
 QY 2 GTTCCT 61
 DB 7 GTTCCT 66
 QY 62 CAATGAGGCGGGGTTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 121
 DB 67 CAATGAGGCGGGGTTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 126
 QY 122 TGGTTTGAAGAGAGTCTGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181
 DB 127 TGGTTTGAAGAGAGTCTGCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 186
 QY 182 GCGGAGCATGCGGAGAGAGCTTGAAGAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241

Db 187 GCGGACATCGCGAGAGAGCTTGAGAGAGCCCTCCGGAAACGGACACGCCGAGCTT 246
QY 242 CCTTGAAGAGAGGGCTGTAAACCCGGGACAGAGAGCCGCAATCGAGAGAGAGG 301
Db 247 CCTTGAAGAGAGGGCTGTAAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGG 306
QY 302 TTGCTTGAAGAGAGCTTGTATGATCATATATCAACAGAGAGAGAGAGAGAGAGG 361
Db 307 TTGCTTGAAGAGAGCTTGTATGATCATATATCAACAGAGAGAGAGAGAGAGAGG 366
QY 362 TTGCTTGAAGAGAGCTTGTATGATCATATATCAACAGAGAGAGAGAGAGAGAGG 419
Db 367 TTGCTTGAAGAGAGCTTGTATGATCATATATCAACAGAGAGAGAGAGAGAGAGG 426
QY 420 TTGCTTGAAGG 478
Db 427 TTGCTTGAAGG 486
QY 479 GCGGCG--GAGCGGAGATTTGCTGTTG--TGACAGAGCTCC--GGGAGAGAGAGAGAGG 534
Db 487 GCGGCGGAGG 546
QY 535 ATCCCTGCGCC--GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 592
Db 547 ATCCCTGCGCC--GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 603
QY 593 TCCCTTGAAGG 652
Db 604 TCCCTTGAAGG 661
QY 653 AANACAGATGAGG 697
Db 662 AANACAGATGAGG 706

RESULT 10
AAC36622
ID AAC36622 standard; DNA; 1633 BP.
XX AAC36622;
AC
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 14477.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
PD
XX
PD 06-SEP-2000.
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 9905-0121825.
PR 05-MAR-1999; 9905-0123180.
PR 09-MAR-1999; 9905-0123548.
PR 23-MAR-1999; 9905-0125788.
PR 25-MAR-1999; 9905-0126264.
PR 29-MAR-1999; 9905-0126785.
PR 01-APR-1999; 9905-0127462.
PR 06-APR-1999; 9905-0128234.
PR 08-APR-1999; 9905-0128714.
PR 16-APR-1999; 9905-0129845.
PR 19-APR-1999; 9905-0130077.
PR 21-APR-1999; 9905-0130449.
PR 23-APR-1999; 9905-0130510.
PR 28-APR-1999; 9905-0130891.
PR 30-APR-1999; 9905-0131449.
PR 9905-0132048.

PR 30-APR-1999; 9905-0132407.
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PR 05-MAY-1999; 9905-0132485.
PR 06-MAY-1999; 9905-0132486.
PR 07-MAY-1999; 9905-0132487.
PR 11-MAY-1999; 9905-0132488.
PR 14-MAY-1999; 9905-0134218.
PR 14-MAY-1999; 9905-0134219.
PR 14-MAY-1999; 9905-0134221.
PR 18-MAY-1999; 9905-0134370.
PR 18-MAY-1999; 9905-0134376.
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PR 21-MAY-1999; 9905-0135353.
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PR 25-MAY-1999; 9905-0136021.
PR 27-MAY-1999; 9905-0136392.
PR 28-MAY-1999; 9905-0136782.
PR 01-JUN-1999; 9905-0137222.
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PR 14-JUN-1999; 9905-0139119.
PR 16-JUN-1999; 9905-0139452.
PR 16-JUN-1999; 9905-0139453.
PR 17-JUN-1999; 9905-0139492.
PR 18-JUN-1999; 9905-0139454.
PR 18-JUN-1999; 9905-0139455.
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PR 18-JUN-1999; 9905-0139461.
PR 18-JUN-1999; 9905-0139462.
PR 18-JUN-1999; 9905-0139463.
PR 18-JUN-1999; 9905-0139750.
PR 18-JUN-1999; 9905-0139753.
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PR 01-JUL-1999; 9905-0142154.
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PR 19-JUL-1999; 9905-0144333.
PR 19-JUL-1999; 9905-0144334.
PR 19-JUL-1999; 9905-0144335.
PR 20-JUL-1999; 9905-0144352.
PR 20-JUL-1999; 9905-0144632.
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PR 21-JUL-1999; 9905-0144814.
PR 21-JUL-1999; 9905-0145086.

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PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145291.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
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PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147132.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
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PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 13-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
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PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 16-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.

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PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 21.0%; Score 169.4; DB 21; Length 1633;
 Best Local Similarity 63.5%; Pred. No. 4.6e-40;
 Matches 304; Conservative 0; Mismatches 168; Indels 7; Gaps 4;

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QY 274 GAGCCGAGTCGACGACCCGAGAGGTTGCTTCGACGCTTCATGACCATATATCAAC 333
D 243 GACATGACAGTTGAGAACCCAGATGAGTCGCTCCATGGTGACATGACATTCGAAC 302
QY 334 AGCAGGCTGCGAGATCTGCTATCTGTCGCGCGCTGACGCAACCGATCGACGAC 393
D 303 AGCAGAGGCGAGAGATTTAGTTACTTCTCTCGCCACCGCAACCCAAATCGAGAT 362
QY 394 TGTGCGGCTGCGACCCCTGATTTGCGATGTCACAGAAAAAGCTGCTGACTGGCGATT 453
D 363 TGTGCGGCTGCGACCCCAATATGCGACCTCGTCGCAAGGTTAGCCGATGCTCATC 422
QY 454 GCGTTTGACGCAACGCAATATGTCGCGGAGCGGGAATTTGTTGTTGACAGATC 513
D 423 GGATTTGCGCAACGCAATCGAGCGCGGAC-GGTCTTTTACGTCGTAACCGACCC 481
QY 514 CGGGAGNATGATCCCGTGAATCCCTGCGCGGGAACACTTANATCCCGTCTCCAA 573
D 482 TGGAGACGACGAT-CCGCTTATATCCATACCGGAGACGTCGTCACGCGGATTC--- 537
QY 574 GAACTGCCCCCTCTGGATCCCTTTAAACNCNANTGAAATCTCNCNANGAGAGA 633
D 538 -AAGAGAACCACTCTGATCATCTTCAAAACCGACATGGTTATTAAC-CTTGAAGCAAGA 595
QY 634 ACTCATTATGACAGCTTTAAACNATGATGACGACNCGTGTCTGTCACATTCGCAA 693
D 596 GCTGATCATGAAAGCTTCAAAACCATGATGTCGTGTCTCATATGTTACATTCGCTAA 655
QY 694 TGGGCGCTGCTGACCAACCAATTTCTCCCAACNCTCTCNCNANGCCTCNCGCC 752
D 656 TGGAGCTTGTCTCAAGTTACATTAAGTTAGATTAATTTGTCATGGATTCATGTC 714

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RESULT 11
AAV69449 standard; cDNA; 823 BP.
AAV69449;
AC 15-MAR-1999 (first entry)
XX
XX Banana fruit ripening-related clone U-51 cDNA.
DE
XX Fruit ripening; banana; modulator; tissue senescence; crop; plant;
KW triploid; plant breeding; ss.
XX
XX Musa acuminata.
OS
XX
XX W09853085-A1.
PN
XX
XX

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OY 574 GAAGTGGCCCTGCGGATCCCTTTAAACNMCNANTGGAATCTCNCCTNANGAAGA 633
 DB 502 AA-----GAACCATATGATGCTCTTTAAACGATGATGATCAACA-TTAAAGNAGA 556
 OY 634 ACTCTTTGAGACAGCTTTAAACNATGATGACNCTGCTCCTGATATGCGCA 693
 DB 557 ACTAATCATGAACAGCTTCAAAACATGATGCTGCGGCTCAAGTTCACATAGCTAA 616
 OY 694 TGGCGCTGCTCCTGACCAACCAATTTCTCCCAACNTCTTCTCCNTGCTCNCCTCC 753
 DB 617 TGGTCATGATATCAGATTCAGATTCGCTGATCAATTAATCATTCATTCGATTCATATCA 676
 OY 754 CAAT 757
 DB 677 TGAT 680
 RESULT 13
 AAV69445
 ID AAV69445 standard; cDNA; 749 BP.
 AC AAV69445;
 XX 15-MAR-1999 (first entry)
 DE Banana fruit ripening-related clone U-11 cDNA.
 XX Fruit ripening; banana; modulator; tissue senescence; crop; plant;
 KW triploid; plant breeding; ss.
 XX Musa acuminata.
 OS W09853085-A1.
 XX 26-NOV-1998.
 PD 05-MAY-1998; 98WO-GB01297.
 XX 20-MAY-1997; 97GB-0010370.
 PR (ZENEC) ZENEC LTD.
 PA
 PI Bird CR, Medina-Suarez RDJ, Seymour GB;
 DR WPI; 1999-059745/05.
 XX
 PT New method of modulating fruit ripening or tissue senescence
 PT characteristics of Musa plants - by introducing DNA sequences,
 PT useful in processes for modifying plant/fruit ripening
 PT characteristics
 PS Claim 1; Page 21-22; 78pp; English.
 CC AAV69440-V69512 are cDNA sequences which are used in a method to
 CC modulate the fruit ripening or tissue senescence characteristics of Musa
 CC acuminata (banana) plants. The method provides a recombinant way of
 CC modulating ripening/senescence characteristics of bananas, which are a
 CC globally important crop. In particular, the method can modulate such
 CC characteristics in the desert banana, which due to its triploid nature
 CC is unaffected by conventional plant breeding techniques.
 CC
 SO Sequence 749 BP; 157 A; 245 C; 197 G; 128 T; 22 other;
 Query Match 17.9%; Score 144.4; DB 20; Length 749;
 Best Local Similarity 64.0%; Pred. No. 9.4e-33;
 Matches 275; Conservative 0; Mismatches 147; Indels 8; Gaps 5;
 OY 325 ATAATCAACAGCAGCTGCGAGATCTCTGTTATCTGCTGCGGTTCAAGCAACCG 384
 DB 135 AGAAGCTTGAACGCTGCTCGCGGAGCTGGGCTCTGATGCGGACGCAACATCG 194
 OY 385 ATCGACGACCTGCTGCGGCTGCGACCTGATTCGATTCACAGAAAAAGCTGCTGAC 444

DB 195 ATCGACGACTGCTGCGGCTGCGACCTGACTGGCTGACAAACCGGACGCTCGTGAC 254
 OY 445 TCGGCATTTGGCTTGGAGCAGCAGCNATANGTGGCCCGAGCGGAATTTGCTGT 504
 DB 255 TCGGCATTTGGCTTGGAGCAGCAGCNATANGTGGCCCGAGCGGAGATTAATGCT 313
 OY 505 GACAGACTCGCGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 564
 DB 314 GACGACAGTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 372
 OY 565 TCTTCCAGAGAGTTGCCCCCTCTGAGATCCCTTTAAACNMCNANTGGAATCTCNC 624
 DB 373 TCAATC---AGAGAGACCCGCTGATGATCAATCTTCAAGCGGACATGCTATCCAGCTG 428
 OY 625 NANGAAGA--CTCNTATGAGACAGCTTTAAACNATGATGACNCTGCTCCTGCTC 683
 DB 429 AAGGAGAGAGCTCATCATGAACTCCACAGACCATGACGCGCGGCGGACGCTCC 488
 OY 684 ACATTTCCCAATGCGCGCTGCTGACCAACCAATTTCTCCCAACNTCTTCTCCTG 743
 DB 489 ACATCTCGGCGGCGCGCTGATCACCATCC-AGTAGTACACCAACATCTCATCCAGCG 547
 OY 744 CTCCTCTGCC 753
 DB 548 GTCCACATCC 557
 RESULT 14
 AAV28659
 ID AAV28659 standard; cDNA; 842 BP.
 AC AAV28659;
 XX 29-JUL-1998 (first entry)
 DE Ripening banana pulp cDNA clone U-0115 SEQ ID NO:17.
 XX Banana; ripening; pulp; Musa acuminata cv. Grand Nain; fruit;
 KW genetic control; tissue senescence; ss.
 XX Musa acuminata.
 OS W09811228-A2.
 XX 19-MAR-1998.
 PD 08-SEP-1997; 97WO-GB02424.
 XX 25-APR-1997; 97GB-0008366.
 PR 10-SEP-1996; 96GB-0018862.
 XX (ZENEC) ZENEC LTD.
 PA
 PI Bird CR, Medina-Suarez RDJ, Seymour GB;
 DR WPI; 1998-207389/18.
 XX
 PT Modulation of ripening or tissue senescence in bananas - comprises
 PT use of DNA isolated from ripening banana pulp to produce genetically
 PT modified fruit
 PS Claim 1; Page 28-29; 72pp; English.
 CC The present sequence represents a cDNA clone isolated from ripening
 CC banana pulp. 57 clones were isolated and are given in AAV28643 to
 CC AAV28659. The cDNA clone sequences can be used in a method of modulating
 CC ripening or tissue senescence processes in plants of the genus Musa. The
 CC method comprises: (a) inserting into the plant material at least 1 of the
 CC 57 sequences (as above); (b) regenerating the plant material, and (c)
 CC selecting from the transformed regenerants, plants with modulated
 CC ripening or tissue senescence characteristics. Also described in the
 CC present invention are: (1) plants, their progeny, seed and material

CC obtained from the plants, produced by the above method; (2) a vector
 CC functional in plants comprising a promoter region which is operably in
 CC plant cells, a polynucleotide sequence as defined above, and a
 CC transcription termination sequence; and (3) a method of controlling
 CC plant pathogens comprising the application of anti-pathogenic agent to
 CC plants of (1).

XX Sequence 842 BP; 177 A; 277 C; 218 G; 154 T; 16 other;

Query Match 17.7%; Score 142.8; DB 19; Length 842;
 Best Local Similarity 64.3%; Pred. No. 3e-32;
 Matches 276; Conservative 0; Mismatches 144; Indels 9; Gaps 5;

QY 325 ATATACACAGCAGCGCTCGCAGATCTTGGTATCTGTGTGCGGTTGAGCAACCG 384
 DB 140 AGAAGCTTGAACGTGCGCGCGCGCGCGCGCTACTTGTCAAGCGGACCGGCAATCCG 199
 QY 385 ATGACGACCTGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 444
 DB 200 ATGACGACCTGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 259
 QY 445 TCGCGCATGCGTGGTGGACGCAACGCNATPANGTGGCGCGCGCGCGCGCGCGCGCG 504
 DB 260 TGGGCGCATGCGGTTGGGAGAAAGCGATTTGGGGCGAGGCGCGCGCGCGCGCGCG 318
 QY 505 GACAGACTCGGCGGACNATATCCCGTGAATCCTGCGCGCGGAGAACATTAAATACCCG 564
 DB 319 GACCGACAGTGGCGGACNACGA-CCCGCTCAATCCGAAAGCGGCGCGCGCGCGCG 377
 QY 565 TCTATCAANAAGTGGCG 624
 DB 378 TCAATCC---AGAGAGAGCGCGGTGGATCATCTTCAAGCGCGCATGATCATCAAGT- 432
 QY 625 NANGAAGAACTGNTTATGAACAGCTTTAANACNATGATGACNCGTGTCTCTGCTCA 684
 DB 433 GAAGAGAGAGCTCATATGAACCTCCCAAGACCATGAGCGCGCGCGCGCGCGCGCGCA 492
 QY 685 CATTCGCAATGCGCGCTGCTGCTCAACNACCAATTTCCCAACNTCTTCTCCNTNGCC 744
 DB 493 CATCTCGGCGGCG 550
 QY 745 TCCNCTGCC 753
 DB 551 TCCACATCC 559

RESULT 15

AAV69448 standard; cDNA; 708 BP.

AAV69448;

15-MAR-1999 (first entry)

Banana fruit ripening-related clone U-31 cDNA.

Fruit ripening; banana; modulator; tissue senescence; crop; plant;
 triploid; plant breeding; ss.

Musa acuminata.

WO9853085-A1.

26-NOV-1998.

05-MAY-1998; 98WO-GB01297.

20-MAY-1997; 97GB-0010370.

(ZENEC) ZENEC LTD.

BIRD CR, Medina-Suarez RDJ, Seymour GB;

DR WPI; 1999-059745/05.

XX New method of modulating fruit ripening or tissue senescence
 PT characteristics of Musa plants - by introducing DNA sequences,
 PT useful in processes for modifying plant/fruit ripening
 PT characteristics

XX Claim 1; Page 23; 78pp; English.

XX AAV69440-V69512 are cDNA sequences which are used in a method to
 CC modulate the fruit ripening or tissue senescence characteristics of Musa
 CC acuminata (banana) plants. The method provides a recombinant way of
 CC modulating ripening/senescence characteristics of bananas, which are a
 CC globally important crop. In particular, the method can modulate such
 CC characteristics in the desert banana, which due to its triploid nature
 is unaffected by conventional plant breeding techniques.

XX Sequence 708 BP; 140 A; 225 C; 192 G; 134 T; 17 other;

Query Match 17.5%; Score 141.4; DB 20; Length 708;
 Best Local Similarity 60.3%; Pred. No. 7.2e-32;
 Matches 290; Conservative 0; Mismatches 182; Indels 9; Gaps 5;

QY 325 ATATACACAGCAGCGCTCGCAGATCTTGGTATCTGTGTGCGGTTGAGCAACCG 384
 DB 137 AGAAGCTTGAACGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 196
 QY 385 ATGACGACCTGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 444
 DB 197 ATGACGACCTGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 256
 QY 445 TCGCGCATGCGTGGTGGACGCAACGCNATPANGTGGCGCGCGCGCGCGCGCGCGCG 504
 DB 257 TGGGCGCATGCGGTTGGGAGAAAGCGATTTGGGGCGAGGCGCGCGCGCGCGCGCG 315
 QY 505 GACAGACTCGGCGGACNATATCCCGTGAATCCTGCGCGCGGAGAACATTAAATACCCG 564
 DB 316 GACCGACAGTGGCGGACNACNA-CCCGCTCAATCCGAAAGCGGCGCGCGCGCGCG 374
 QY 565 TCTATCAANAAGTGGCG 624
 DB 375 TCAATCC---ANAGAGAGCGCGGTGGATCATCTTCAAGCGCGCATGATCATCAAGT 430
 QY 625 NANGAAGAACTGNTTATGAACAGCTTTAANACNATGATGACNCGTGTCTCTGCTCA 684
 DB 431 AAGAGAGAGCTCATATGAACCTCCCAAGACCATGAGCGCGCGCGCGCGCGCGCGCA 490
 QY 685 CATTCGCAATGCGCGCTGCTGCTCAACNACCAATTTCCCAACNTCTTCTCCNTNGCC 743
 DB 491 CATCTCGGCGGCG 550
 QY 744 CTCGCGC---TCCCAATGCAACCCGCGGAAATTCGTCGCGCGCGCGCGCGCGCGCG 801
 DB 551 GTCCACATCAGACGATGCAATCCANGCGGAGAACTCTCTGTTGCGCACTCCCGCATNG 610
 QY 802 G 802
 DB 611 G 611

Search completed: June 24, 2003, 00:50:33
 Job time : 254 secs



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 23:50:47 ; Search time 1449 Seconds
(without alignments)
9008.670 Million cell updates/sec

Title: US-09-966-881-13

Perfect score: 806
Sequence: 1 TGTCTCTCTCTGATACACA.....TCCCTCTCTCTATGATNG 806

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:*
1: em_estda:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pla:*
21: em_gss_vtl:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	185	23.0	501	9	AI770665
2	176	21.8	480	9	AJ469163
3	173.6	21.5	589	17	AZ135244
4	170	21.1	595	14	BO741525
5	169.2	21.0	462	17	BH874844
6	166	20.6	800	14	BQ999911

7	165	20.5	720	14	BQ870176	BQ870176	QGD8F08.y
8	164.4	20.4	784	17	AZ916009	AZ916009	Est1.1.hi
9	162.4	20.1	685	14	BO795866	BO795866	EST 4804
10	150	18.6	632	13	BI959076	BI959076	HVSMER001
11	149.4	18.5	679	10	AV822011	AV822011	AV822011
12	149.2	18.5	883	10	BE035831	BE035831	MO10611.M
13	144.8	18.0	612	14	BO148154	BO148154	NE062C07F
14	143.8	17.8	420	14	BO134100	BO134100	san57c10.
15	141.2	17.5	518	14	BO104182	BO104182	fc2443.e
16	141	17.5	365	12	BF655654	BF655654	PM1 47.B1
17	140.2	17.4	634	10	AW223193	AW223193	EST300004
18	139.8	17.3	789	12	BG599600	BG599600	EST504495
19	138.8	17.2	341	10	AW398301	AW398301	EST298148
20	133.8	16.6	632	14	BO148911	BO148911	NE084D12F
21	130.4	16.2	541	10	AV527067	AV527067	AV527067
22	130.2	16.2	542	12	BG040772	BG040772	NXSI 114
23	130	16.1	629	10	AV827058	AV827058	AV827058
24	129.6	16.1	620	10	AV825500	AV825500	AV825500
25	126.6	15.7	539	10	AV527181	AV527181	AV527181
26	126.4	15.7	727	14	BO634030	BO634030	AV442702
27	125.8	15.6	362	10	AV420958	AV420958	NXRV063.H
28	124.4	15.4	635	14	BO700242	BO700242	AV420958
29	124.2	15.4	609	17	BH717800	BH717800	NXRV103.B
30	123.6	15.3	515	14	BO634633	BO634633	BO634633
31	122.4	15.2	682	13	BI924648	BI924648	EST544537
32	122.4	15.2	686	14	BO401767	BO401767	CA_Bd004
33	122.4	15.2	686	14	BO401767	BO401767	CA_Bd004
34	122.4	15.2	764	17	BH583673	BH583673	BOH209TF
35	121.4	15.1	436	12	BG319625	BG319625	SD8B12.S0
36	120.4	14.9	786	17	BH647126	BH647126	BOMB52TF
37	120.2	14.9	605	12	BG045860	BG045860	aaa07c02.
38	119.4	14.8	666	12	BG599297	BG599297	EST504197
39	117.4	14.6	666	12	BO508106	BO508106	EST615521
40	117.4	14.6	773	14	BO699768	BO699768	NXRV128.F
41	116	14.4	728	14	BM492945	BM492945	NXRV_032
42	115.4	14.3	473	13	BF008833	BF008833	ss70a05.y
43	115	14.2	644	10	AW683073	AW683073	NF007A12L
44	114.8	14.2	567	13	BI471247	BI471247	sa895b04.
45	114	14.1					

ALIGNMENTS

RESULT 1
LOCUS AI770665 501 bp mRNA linear EST 02-FEB-2000
DEFINITION 606055G03.x2 606 - Ear tissue cDNA library from Schmidt lab zea
Mays CDNA, mRNA sequence.

ACCESSION AI770665
VERSION AI770665.1 GI:5268701
KEYWORDS EST.

SOURCE zea mays.

ORGANISM zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 501)

AUTHORS Walbot,V

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 606055 row: G column: 03.

FEATURES
source location/Qualifiers
1..501
/organism="Zea mays"

/cultivar="Ohio43"
 /db_xref="taxon:4577"
 /clone_1lb="606 - Ear tissue cDNA library from Schmidt
 lab"
 /tissue_type="mixed"
 /dev_stage="ear length from 0.5 cm - 2.0 cm"
 /lab_host="XLOLR (Stratagene)"
 /note="Organ: Immature ear; Vector: pBK-CMV; Site:1: EcorI
 ; Site:2: XhoI; Mixed ear tissue cDNA library from Schmidt
 lab"
 BASE COUNT 111 a 178 c 137 g 75 t
 ORIGIN

Query Match 23.0%; Score 185; DB 9; Length 501;
 Best Local Similarity 69.2%; Pred. No. 8.7e-45;

Matches 306; Conservative 0; Mismatches 128; Indels 8; Gaps 5;

QY 312 GGTCTGATGACCAATATCAACAGACGGCTGCGAGATCTGTGTTATCTCTCGTGGG 371
 DB 6 GCTCTGACAGTTCATCAACACATCAACGCGCCGCGAATCTCGGTACTCTGTCGGG 65
 QY 372 TTCAGCAACCCGATCGAGAGTGTGGCGGTGCGACCTGATGTCATGTCACAGAAA 431
 DB 66 GACAGCAACCCGATCGAGAGTGTGGCGGTGCGACCTGATGTCATGTCACAGAAA 125
 QY 432 AAAGCTGCTGACCTGCGCATGTGCTTGGAGCAACGATATGATGCGCGGAGGAGA 491
 DB 126 GCGCTCCGCGCATGTGCGCATGTGCGCGGAGCAACGATGCGCGGAGGAGC-GGCA 184
 QY 492 ATTTGTGTTGTGACAGACTCGGGGACNATGATCCCGTGAATCTCTGCGCGGAGAAA 551
 DB 185 AGATCTAGTGTGTCACACACGCGAGATGACGA-CCCTGTACACCGCGCAAGGCGACC 243
 QY 552 CTTANATACCCGCTGCTCCGAGAAAGTGGCCCTGCGGATCCCTTTAAACNCAANT 611
 DB 244 CTCCCTACGCGCATGTCAGGAA----GAGCGGTGTCGATCATCTTCAACGCGGAGAT 299
 QY 612 GGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 671
 DB 300 GGTCTGACAGCTC-AAGAGAGAGTCTATCATGTAAGCTTCAAGCACTGACGAGCGG 358
 QY 672 GTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731
 DB 359 GCGCAAGCTGACATGCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 417
 QY 732 TTTCTTCNTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 753
 DB 418 ATCATCCAGCGGCTCCACATCC 439

RESULT 2
 LOCUS AJ469163 480 bp mRNA linear EST 24-MAY-2002
 DEFINITION AJ469163 Hordeum vulgare cDNA clone S0000800244H10F1, mRNA
 sequence.
 ACCESSION AJ469163
 KEYWORDS EST.
 SOURCE Hordeum vulgare.
 ORGANISM Hordeum vulgare.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 ; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 480)
 AUTHORS Saven, A.-M., Tanskanen, J., Paulin, L. and Schulman, A.H.
 TITLE Barley EST's
 JOURNAL Unpublished (2002)
 COMMENT Contact: Schulman AH
 Institute of Biotechnology
 University of Helsinki
 P.O.Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014,
 Finland.

FEATURES Location/Qualifiers

source 1. .480
 /organism="Hordeum vulgare"
 /db_xref="taxon:4513"
 /clone="S0000800244H10F1"
 /clone_1lb="S00008"
 /tissue_type="callus"
 /note="Callus K19"
 BASE COUNT 102 a 175 c 134 g 69 t
 ORIGIN

Query Match 21.8%; Score 176; DB 9; Length 480;
 Best Local Similarity 68.2%; Pred. No. 4.5e-42;

Matches .300; Conservative 0; Mismatches 132; Indels 8; Gaps 5;

QY 314 TCCGTATGACCAATATCAACAGACGGCTGCGAGATCTGTGTTATCTCTCGTGGG 373
 DB 14 TCCGTATGACCAATATCAACAGACGGCTGCGAGATCTGTGTTATCTCTCGTGGG 73
 QY 374 CAGCAACCCGATCGAGAGTGTGGCGGTGCGACCTGATGTCATGTCACAGAAA 433
 DB 74 CCGGCAACCCGATCGAGAGTGTGGCGGTGCGACCTGATGTCATGTCACAGAAA 133
 QY 434 AGCTGCTGACCTGCGGCAATGCTTGGACGACGATATGTCGCGCGGAGAT 493
 DB 134 GCTTCCGCGATCTGCGGCAATGCTTGGACGACGATATGTCGCGCGGAGAT 192
 QY 494 TTGTTGTTGTGACAGACTCGGGGACNATGATCCCGTGAATCTCTGCGCGGAGAACT 553
 DB 193 ATCTACGTTGTGACAGACTCGGGGACNATGATCCCGTGAATCTCTGCGCGGAGAACT 251
 QY 554 TATATACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613
 DB 252 GCGCTACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 307
 QY 614 AAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 673
 DB 308 TCATACACCTC-AGCAGAGAGTCTATCATGTAAGCTTCAAGCACTGACGAGCGG 366
 QY 674 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 733
 DB 367 GCCAAGCTGACATGCGCAAGCGCGCTGATCATCACATCC-AGTACGTACCAAGCTCAT 425
 QY 734 CTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 753
 DB 426 CATCCAGCGGCTCCACATCC 445

RESULT 3
 LOCUS AZ135244 589 bp DNA linear GSS 02-JUN-2000
 DEFINITION OSJNB0115A18r CUGI Rice BAC library (EcorI) Oryza sativa genomic
 clone OSJNB0115A18r, DNA sequence.
 ACCESSION AZ135244
 KEYWORDS GSS.
 SOURCE Oryza sativa.
 ORGANISM Oryza sativa.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Eubartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 589)
 AUTHORS Wing, R.A. and Dean, R.A.
 TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
 JOURNAL Unpublished (1998)
 COMMENT Contact: Wing RA
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Seg primer: GGAAACAGCTATGACATG
 Class: BAC ends

High quality sequence start: 21
High quality sequence stop: 547.
Location/Qualifiers

1. 589
/organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="OSJNB0115A18r"
/clone_1lb="CUGI Rice BAC Library (EcoRI)"
/tissue_type="leaf"
/lab_host="E. coli DH10B"
/note="Vector: pBACindigo; Site_1: EcoRI; Site_2: EcoRI;
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mbp (Arumuganathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
we have constructed a BAC library from Oryza sativa,
Nipponbare variety using EcoRI as the cloning enzyme. The
library contains 55,296 clones with an average insert size
of 121 Kb providing approximately 15 haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99.9 %. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."

BASE COUNT 121 a 203 c 171 g 91 t 3 others
ORIGIN

Query Match 21.5%; Score 173.6; DB 17; Length 589;
Best Local Similarity 68.1%; Pred. No. 2,7e-41;
Matches 297; Conservative 0; Mismatches 131; Indels 8; Gaps 5;

314 TCCTGATGACCATATCAACAGCAGCGCTGCGAGATCTGGTATCTGTCGGGTT 373
1 TCATCAGGTGATCAGACAGCAGCGCGAGAGAACTGGCTACCTCTGTCGGCA 60
374 CAGGCAACCCGATGACGAGCTGCTGGCGTGCAGCCCTGATGGCATGTCAAGAAAA 433
61 CCGGCAATCGATGACGAGCTGCTGGAGTGGCAGCCGAGATGCAACAATGCCAGC 120
434 AGCTCGTACCTGCGGCGATGGCTTTGGACCAACGCNATANGTGGCCGCGAGGAT 493
121 GGCTCGCGGAGTGGGATGGCTTGGCGGCAAGCCATCGCGCGGAC-GGCAG 179
494 TTGTGTGTGACAGATCGCGGAGCNATATCCCGTGAATCTTCCCGGGAACACT 553
180 ATCTAGTGTACACCGACCCGAGGAGACGA-CGGGTAAACCCCAAGAGGGCAGCT 238
554 TAAATACCCGCTNTCCANGAAGTTGCCCTCTGTGGATCCCTTTAAACNNAATGG 613
239 CCGGTAGCGCGTATCC---GGGAGAGCGCGCTGTGATCGTCTTAAACGCAATGG 294
614 AATCTGCTCNCNANGAAGATCTNTATGACAGCTTTAANACNATGATGACNCGT 673
295 TGATCAGAGCTC-AAGGAGAGCTGATCATGACAGCTTCAAGACATGAGCGCGTGGC 353
674 GTCTCGTCCACATTTGACATGGGCGCTGCTGNTCAACNCAATTTCTCCCAACNCTT 733
354 GCCAAGTGCATTCGCCAATGGCGCTGATCAGCATTC-AGTACGTCAACAGCTCAT 412
734 CTTCNTNCCCTCCNC 749
413 CATTCATGGCGCTGAC 428

RESULT 4
B0741525
LOCUS
DEFINITION
seq1911.y1 Gm-cl045 Glycine max cDNA clone SOYBEAN CLONE ID: 5'
Similar to TR:024416 024416 PECTATE LIASE. ; mRNA sequence.
ACCESSION
B0741525
VERSION
B0741525.1 GI:21888312
KEYWORDS
EST.
SOURCE
soybean.
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE
1 (bases 1 to 595)
Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Corryell, V., Khanna
, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers
, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
, R., Waterson, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: cure@resgen.com web site:
www.resgen.com

Seq primer: -40RP from GIBCO
High quality sequence stop: 430.
Location/Qualifiers

FEATURES
source

1. 595
/organism="Glycine max"
/db_xref="taxon:3847"
/clone_1lb="Gm-cl045"
/tissue_type="Hypocotyl, 9-10 day old etiolated seedlings"
/lab_host="DH10B"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from etiolated hypocotyl tissue of 9-10 day old seedlings
of the cultivar Williams 82. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) primer with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by digestion with EcoRI and XhoI. The cDNA
fragments were directionally cloned into the EcoRI-XhoI
restriction site of the pBluescript vector. The ligated
cDNA fragments were transformed into DH10B host cells
(Gibco BRL). This library was constructed by Dr. Randy
Shoemaker."

BASE COUNT 149 a 171 c 169 g 106 t
ORIGIN

Query Match 21.1%; Score 170; DB 14; Length 595;
Best Local Similarity 63.7%; Pred. No. 3.3e-40;
Matches 307; Conservative 0; Mismatches 168; Indels 7; Gaps 4;

236 ATCTTCTTGGAAAGAGGCGTGTACCCGGGAGAGAAAGCCGAGTGCAGACCCG 235
117 ATTGCTAAATGGAGAAAGGTTCAGGGAGTCTTGAATGAACATGCGATGATTAATCCAG 176
296 AGGAGTTGCTTGCAGCGCTCATGATCAATTAACACAGCAGCGCTCGAGATCTTG 355
177 AGGAGATTTGCTTCATGTTGATGAGAGCATACGCAACTACAGGCTCGAAGAACTGA 236
356 GTTATCTGTGTGGGTTCAAGGCAACCCGATGACGACTGCTGGCGGTGACCCCTGATT 415


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Db      237  ACTTCTTTCATGCGGGGTCCGGGAACCAATCGAGGACTGCTGGGGGTCCGCAAGCGGT 296
OY      416  GGCATGTCAAACGAAAAAGCTGCGTGACTGGGGATTTGGCTTTGGAGCCAAACGCAATAN 475
Db      237  GGTACGCCCGCCGCAAGCGCTTAGCAACTGGGATCGGTGGTGGCCGAACGGCCATCG 356
OY      476  GTGGCCGGGAGCGGGGAATTTGTTCTGTTGACAGACTCCGGAGCAANATGATCCCGGTGA 535
Db      357  GCGGCGCGGAC- GGGCGCTACTAGCTGCTGTGGACCCGGGAGAGAGA- CCGAGTCAA 414
OY      536  TCTCTGCCCCGGGACACTTANATACCCCGCTCMTCCANAGAGTTGCCCTCTGGGATCC 595
Db      415  CCGCAACCCGGCACCTCTCCGGCAGCGGTGATCCAGGACG- - - - -CCCCCTCTGGATCG 470
OY      596  CCTTTAAACNCAANTGTAATCTGCTGCTCNANAGAAAGCACTGTTATGAACGCTTTAN 655
Db      471  TGTTCAGAGCGGACATGTGTCATTAAC-CTTTAAAGCAAGAACTCATATGACAGCTTCAAG 529
OY      656  ACNATCGATGAGCANCNGTGTCTCGTCCACATTTGCCATGGCGCTGCTGCACCANCAA 715
Db      530  ACCATCGAGGCGCGGCGGTGAAAGTCCACATCGCTTATGGTGGCTGATCACCATTACG 589
OY      716  TT 717
Db      590  TT 591

```

RESULT					
BH874844/c					
LOCUS	BH874844	462 bp	DNA	linear	GSS 05-AUG-2007
DEFINITION	hg22a06.b1 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays genomic clone hg22a06 5', DNA sequence.				

ACCESSION	BH8/4844
VERSION	BH874844.1
KEYWORDS	GSS.
SOURCE	Zea mays.
ORGANISM	Zea mays

REFERENCE	TITLE
<p> AUTHORS Rabinowicz, P. D., O'Shaughnessy, A. L., Bailja, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, R., Nascentino, L., Zaveren, T., McComble, W. R. and Martienssen, R. A. </p>	<p> TITLE Genomic shotgun sequences from <i>Zea mays</i> (methyl-filtered) </p>
<p> COMMENT Unpublished (2002) Contact: W. Richard McComble </p>	<p> REFERENCE 1 (bases 1 to 462) Rabinowicz, P. D., O'Shaughnessy, A. L., Bailja, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, R., Nascentino, L., Zaveren, T., McComble, W. R. and Martienssen, R. A. </p>

FEATURES
 source
 1. .462
 Location/Qualifiers
 High quality sequence stop: 462.

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/organism="zebra_mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="hg82a06"
/clone_1lb="WGS-zmaysF (JM107 adapted methyl filtered)"
/lab_host="JM107 or DH5a"
/notes="Organ: immature ears; Site_1: Xba I; Site_2: Xba I"
The vector was digested with XbaI and one nucleotide was
added by fill in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(x/y reads in M13mp19, b/g reads in pUC19). The same

```

BASE COUNT	59 a	150 c	159 g	94 t	
ORIGIN	ligation was transformed in either JM107 or DH5a. "				
Query Match	21.0%	Score 169.2	DB 17	Length 462	
Best Local Similarity	69.5%	Pred. No. 5.1e-40			
Matches 283	Conservative 0	Mismatches 116	Indels 8	Gaps 5	

OY	347	GATCTCTTGGTTATCTGTGTCGTGCAGGCCAACCCGATGACGACACTGCTGGCGGTGCG	406
Dd	462	GAAACCTCTGGGTACTCTGCTGTGCGGGACAGCACAACCCTCATGCACACTGTGGCCCTGCG	403
OY	407	AOCCTGATTTGGCATGTCTCAACGAAAAAAGCTCCGTGACTGGGGCATTTGGCTTTGGACCCA	466
Dd	402	ACTGGGACTGGCACAGCAACACGGCACGGCGCTGGCCCCGACTGGCGCATGGGGTTCCGCCCA	343
OY	467	ACGNATAMTGAGGCCGCGACGCGGGGAATTGTTGCTGTTGACAGACTCCGGGGACNAATGAT	526
Dd	342	ACGGCATCGGGGGCGCGGAC--GCGAAGSTGTACGTGTGTGACGACGCCACGACGACACAT	284
OY	527	CCCCGTGAATCTTGCCCCGGGACACTTAATATACCCCGTCNTCCANAAGTTGCCCCCT	586
Dd	283	-CCGCTGAACCCGGCGCGAGGGCACCCCTCCGGACACCCCTCATTC---AGAGAAGAGCGCG	229
OY	587	CTGGGATCCCCTTTAAACNCNAANTGGAATCTCTCNANAGSAAGACTNTATGAA	646
Dd	228	TGTGGATCATTTCAAGCGGGACATGTTGATCAAGCT-GAAGGAGAACTCATCTAGAAC	170
OY	647	AGCTTAAACNATCGATGACNCGTGTCTCTGTCACATTTGCCATGGGCGCTGCTATC	706
Dd	169	AGCTTCAAGACCATTCGAGCGGCGGGGCCCAACGTCACATTCGCCCAACGGGCGCTCGCTC	110
OY	707	ACCANCAATTTCTCCCAACACTTCTTTCGCTNGCTCCNCTCC	753
Dd	109	ACCATTC-AGTAGCTGACCAAGCTCATCATCCAGGGGTCTCCACATTC	64

RESULT	6
LOCUS	BQ999911
DEFINITION	BQ999911 800 bp mRNA linear EST 22-AUG-2002
ACCESSION	OG623G08.yg.ab1 OG_EFGHT lettuce serritola Lactuca sativa cDNA clone.
VERSION	BQ999911
KEYWORDS	BQ999911.1 GI:22434307
SOURCE	EST.
ORGANISM	Lactuca sativa.
	Lactuca sativa

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 800)	Kozik, A., Michelmore, R. W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., Van Damme, M., Lavelle, D., Chevalier, P., Ziegler, T., Ellison, P., Kolman, J., Slabaugh, M. S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, R.	Letuce and Sunflower ESTs from the Compositae Genome Project	http://compgenomics.ucdavis.edu/	
	Unpublished (2002)			Contact: Alexander Kozik [R.W.Michelmore]

Department of Vegetable Crops, R.W. Michelmore lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95610, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig OG_CA_contig5568, see <http://cgpdb.ucdavis.edu/>
for details.

Plate: OGG23

row: G column: 08.

Location/Qualifiers

1. 800

FEATURES

SOURCE

/organism="Lactuca sativa"
/cultivar="L. serriola"

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/db_xref="taxon:4236"
/clone="QG6233608"
/clone_id="QG_EFGHU lettuce serriola"
/lab_host="E.coli"
/note="Vector: pRCNASTAB: The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpbd.ucdavis.edu/
rAG_SEQ=Not found"

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BASE COUNT	221 a	179 c	207 g	193 t
ORIGIN				

Query Match	20.6%;	Score 166;	DB 14;	Length 800;
Best Local Similarity	64.0%;	Pred. No. 6.3e-39;		
Matches 297; Conservative	0;	Mismatches 160;	Indels 7;	Gaps 4;

QY	274	GAAGCCGCAAGTGCAGACACCCCGAGAGGTTGGTTCGAGCGGTCGATGACATATATCAAC	333
Db	324	GAATAAGCTTTCAGATCTCTGAGGAAGTGGCTCTCATGCGCTGAAATGATATTAATAAAC	383
QY	334	AGCACGGCTCGCAGATCTCTTGGTTATCTGTGTGCGGGTTGAGGCAACCCGATGCAGAC	393
Db	384	AACACGGAAGAAAGAAATACCTCGGATACCTTCATCTGTGGAACCGGAAACCAATGCAGAT	443
QY	394	TGCTGGCGGTGGGACCCCTGATTTGGATGTGCAACAGAAAAAAGCTCGCTGACTGGGGCAT	453
Db	444	TGCTGGCGGTGGGACCCCAACTGGCAAAAAAACCGGAAACGCTCTGGCGACTGGGGATC	503
QY	454	GGCTTTGAGACGCAACGCNATANGTGGCCGCGACGGGGAATTTGGTTGCTGTGCAGACATC	513
Db	504	GGATTTGGCGGGAATGCATGGGAAGTGGCGAC -GGCGGTTATTCATGTGTCACAGATTC	562
QY	514	CGGGGACNATGATCCCCGCGAATCTCGCCCGGGGAACCTTAAATACCCTGCTCCAAAT	573
Db	563	CGCGCGACGACGAT -CCAGTGAACCCACGACACCCGCGACCCCTCGCGACGCGCTCAATTC -	618
QY	574	GAGTTGACCCCTCGTGGATCCCTTTAAACNCAANTGAAATCTCNCNCNANGAAGA	633
Db	619	-AAGATACCCCTCTTTGGATCGTTTCAACGCGCATGGTGAT -TCAATTGAAGCAAGA	676
QY	634	ACTCNTATTGAACAGCTTTAAANACNATGATGAGACNCGTCTCCGTCACATTTGCCAA	693
Db	677	ACTTATTATGAACAGTTTAAACACCATGAGTGTCTGTGAGCATCAATGTTCATATGCGAA	736
QY	694	TGGCGGCTGCTGACCAACCAATTTCTCCTCCCAACNTCTTCTTC	737
Db	737	TGGAGCTGTATTAACGTGATGCTAAATGGTCACTAATAGTATTC	780

RESULT	7
B0870176	
LOCUS	B0870176
DEFINITION	720 bp mRNA linear EST 15-AUG-2007
ACCESSION	OG8BF08.yg.ab1 OG_ABCDI lettuce salinas Lactuca sativa cDNA clone
VERSION	OG8BF08, mRNA sequence.
KEYWORDS	B0870176 B0870176 GI:22256484
SOURCE	EST.
ORGANISM	Lactuca sativa.
	Lactuca sativa

REFERENCE
AUTHORS

1 (bases 1 to 720)
Kozlik, A., Michelmore, R. W., Knapp, S., Matvienko, M., Rieseberg, L., Lin H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison, P., Kolkmann, J., Slabaugh, M. S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.

TITLE lettuce and sunflower ESTs from the Compositeae Genome Project
JOURNAL <http://compgeomomcs.ucdavis.edu/>
COMMENT Unpublished (2002)
Contact: Alexander Kozik [R.W.Mitchelmore]

Lettuce and Sunflower ESTs from the Compositae Genome Project
<http://compgenomics.ucdavis.edu/>
 Unpublished (2002)
 Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Asmundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@ucdavis.edu [michelmoreveg@ucdavis.edu]
 belongs to contig OG_CA.Contig5568, see <http://cgpub.ucdavis.edu/>
 for details.
 Plate: QGD8 row: F column: 08.

FEATURES	Location/Qualifiers
source	1. .720

/organism="Lactuca sativa"
 /cultivar="Salinas"
 /db_xref="taxon:4236"
 /clone="QGD8F08"
 /clone.lib-QG-ABCDI lettuce salinas"
 /lab.host="E.coli"
 /note="Vector: pBKCDNA5flab: The library was constructed
 from 10 different sources of RNA from a single genotype.
 Separate cDNAs were generated using primers that
 incorporated unique 5' and 3' tags to distinguish each
 source of RNA. cDNAs were then pooled, size-fractionated,
 directionally cloned into a custom medium-copy vector and
 transformations made with four size classes to minimize
 size bias. Details of each source of RNA and library
 construction are available at [http://cgpdb.ucdavis.edu/
 tag.lib-QG-ABCDI lettuce salinas](http://cgpdb.ucdavis.edu/tag.lib-QG-ABCDI lettuce salinas)
 TAG_TISSUE=shoots environmental stress
 TAG_SEQ=TCGCAACGGG"

BASE COUNT	201 a	156 c	186 g	177 t
ORIGIN				

Query Match	20.5%	Score 165;	DB 14;	Length 720;
Best Local Similarity	65.2%	Pred. No. 1.2e-38;		
Matches 290; Conservative	0;	Mismatches 148;	Indels 7;	Gaps 4

QY	274	GAAGCCGAGTGGACAGACACCCCGAGGAGGTGGTTGACGGGCTGATGACCATTAATCAC	3333
Db	226	GAAATAGCTTTCAAGATCCTGAGGAAGTGGCTTCATGTTGAATGTATTAATAAAAC	2855
QY	334	AGCACGGCTGCGAGATCTCTTGGTTATCTGTGTCGGGTTCCAGGCAACCCGATGACGAC	3933
Db	286	AACCGGAAAGAAAGAAAACCTCGATACCTTCATGCTATGTGAACCGGAAACCAATGAGCAT	3455
QY	394	TGCTGGCGGTGGGACCCCTGATTTGGCATGTGCACAGAAAAAGCTGCTGACTGGGGCATT	4533
Db	346	TGCTGGCGGTGGACCCCAACCTGGCAAAAAAACCGGAAACCCCTGGCGAGCTGGGGCATC	4055
QY	454	GGCTTTGGAGCGCAACGCNATANGTGGCCGCGACGGGGAAATTGTTGCTTGGACAGACTC	5133
Db	406	GGATTTGGGCGGGATTCGATCGGAAGTGGCGAC -GGCGGTTATTCATAGTGCACAGATTC	4645
QY	514	CGGGGACNATGATCCCCGTAATCTCTCGCCCGGGGAACCTTAATACCCTGCTNTCCAA	5733
Db	465	CGGCGACGACGAT -CCAGTGAACCCACAGACCCGGGACCCCTCGCCAGCGCGTCAATC ---	5205
QY	574	GAAGTGGCCCCCTCGGGATCCCTTTAAACNCNANATGGAATCTCNCNCNANGAAGA	6333
Db	521	-AAGATACCCCTCTTTGGATCGTGTTCACAGCGGACATGGTGGAT -TCAATTGAAGCAGAGA	5785
QY	634	ACTCNTTAAGAACAGCTTTAANACNATGATGGAACNCGTGTCTCTGTCACATTGGCAA	6933
Db	579	ACTTATTATGAACAAGTTTAAAAACATGATGCTGTGTGAGTCAATGTTCATATCGGAA	6385
QY	694	TGGCGCCTGCNTCACCANCAATTT 718	
Db	639	TGGAGCTGTATTACTGTTCAATTT 663	

LOCUS	784 bp	DNA	linear	GSS 15-MAR-2001
DEFINITION	AZ916009	Psst_1_h12-c-1_0 Maize Psst B73 Leaf Zea mays genomic, DNA		
ACCESSION	AZ916009			
VERSION	AZ916009.1	GI:13347280		
KEYWORDS	GSS.			
SOURCE	Zea mays.			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.			
REFERENCE	1 (bases 1 to 784)			
AUTHORS	Missouri Maize Project--Maize Mapping Project.			
TITLE	Psst Zea mays B73 Psst Leaf Lissue Library			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Schroeder S Missouri Maize Project--Maize Mapping Project University of Missouri 209 Curtis Hall, Columbia, MO 65211, USA Tel: 573 882 8214 Fax: 573 884 7850 Email: sschroeder@celephais.agron.missouri.edu Class: shotgun.			
FEATURES	location/Qualifiers			
source	1..784			
	/organism="Zea mays"			
	/cultivar="B73"			
	/db_xref="taxon:4577"			
	/clone_lib="Maize Psst B73 Leaf"			
	/tissue_type="leaf"			
	/lab_host="DH5 alpha"			
	/note="Organ: Leaf; Vector: pUC19; Psst digested B73 genomic sucrose gradient size fractionated fragment sizes of 0.5kb to 2kb ligated to pUC19 transformed in DH5 alpha"			
BASE COUNT	190 a 202 c 210 g 182 t			
ORIGIN				
Query Match	20.4%; Score 164.4; DB 17; Length 784;			
Best Local Similarity	70.0%; Pred. No. 1.9e-38;			
Matches 266; Conservative 0; Mismatches 107; Indels 7; Gaps 4;				
319	ATGACCAATCAACACGACGCGGCGCAGATCTCTGGTTATCTCTGGGTTACAGC	378		
412	AGGTGCATCAGGAACAGCAGCGCCCGGGAACCTCGGTCTCTGCGGACAGCG	471		
379	AACCGATGACGACTGCTGGCGGTGACACCTTGATGTCATGCAACAGAAAAAGCTC	438		
472	AACCGATGACGACTGCTGGCGGTGACACCTTGATGTCATGTCACACACGCGACGGCTG	531		
439	GCTGACTGCGGATGCTTGGAGCGCAACGCMATANTAGTGGCCCGGACGGGAAATTGTT	498		
532	GCCGACTGCGGATGCTTGGAGCGCAACGCMATANTAGTGGCCCGGACGGGAAATTGTT	590		
499	CGTGTGACACATCCCGGCGGCAACGCMATANTAGTGGCCCGGACGGGAAATTGTT	558		
591	CGTGTGACACATCCCGGCGGCAACGCMATANTAGTGGCCCGGACGGGAAATTGTT	649		
559	ACCGCGTCTGCAANGAAGTTGGCCCGCTCTGGATTCCTTTAAACNMANTGGAATC	618		
650	ACCGCGTCTGCAANGAAGTTGGCCCGCTCTGGATTCCTTTAAACNMANTGGAATC	705		
619	TCNCTCNAAGCAAGCACTTATGACAGCTTTAANACNMATGATGACNCTGTCCT	678		
706	ACGCT-GAGGAGAGGAGCTCATCATGAAACGTTTAAAGCATGACAGCGCGCGCCAA	764		
679	CGTCCACATTCGCAATGGCG	698		
765	CGTCCACATTCGCAATGGCG	784		

LOCUS	BO795866	685 bp	mRNA	linear	EST 30-JUL-2002
DEFINITION	BO795866 EST 4804 Ripening Grape berries Lambda Zap II Library Vitis				
ACCESSION	Vitisifera CDNA Rf021D12 3', mRNA sequence.				
VERSION	BO795866				
KEYWORDS	BO795866.1 GI:22010832				
SOURCE	EST				
ORGANISM	Vitis vinifera.				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae; Vitis.				
AUTHORS	1 (bases 1 to 685)				
TITLE	Abbal,P., Agasse,A., Ageorges,A., Anassova,R., Barrieu,F., Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N.				
COMMENT	Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages				
JOURNAL	Unpublished (2002)				
CONTACT	Contact: Romieu C.				
COMMENT	Unité de Recherche des Produits de la Vigne				
COMMENT	Institut National de la Recherche Agronomique				
COMMENT	2, place Viala, 34 060 Montpellier Cedex 01, France				
COMMENT	Tel.: 00-33-(0)4-99-61-28-62				
COMMENT	Fax: 00-33-(0)4-99-61-28-57				
COMMENT	Email: romieu@ensam.inra.fr				
COMMENT	Seq primer: 17.				
FEATURES	Location/Qualifiers				
SOURCE	1..685				
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	/cultivar="Shiraz"				
	/db_xref="taxon:29760"				
	/clone="Rf021D12"				
	/clone_id="Ripening Grape berries Lambda Zap II Library"				
	/dev_stage="ripening stage"				
	/note="Organ: Fruit; Vector: Lambda Zap II; Site.1: Eco RI ; Site.2: XhoI. Oriented library, construction described in Generation of ESTs from grape berry (skin, pulp or seeds) at various developmental stages by Terrier,N., Ageorges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158 (12): 1575-83 2001"				
BASE COUNT	171 a	166 c	180 g	168 t	
ORIGIN					
Query Match	20.1%	Score 162.4;	DB 14;	Length 685;	
Best Local Similarity	62.8%	Pred. No. 7.2e-38;			
Matches 297;	Conservative 0;	Mismatches 169;	Indels 7;	Gaps 4;	
QY	280	GCACGTGCACGACCCCGGAGAGAGTTCCTTCACGCGTCTCCTGATGACCATATCAAGACACG	339		
DB	206	GCAATGTATGACCCAGATGACAGTGGCTTCATGTGTGAGACATGACCATTCGGAAAGACACA	265		
QY	340	GCTCGCAGANTCTCTGGTATCTCTGTCGTGCAGTTCAGGCAACCCGATCGACGATCTGG	399		
DB	266	GAGAGGAAGGAATTAAGTATTATTTCTCGTGTGAACTGTATTCATTGATGATGCTCTGG	325		
QY	400	CGGTGCGACCTGATTTGGCATGTCAAGAAAAAAGCTCGCTGACTCGGGCATTGGCTTT	459		
DB	326	CGATGTGACCAATTTGGCAAAAAGAACCGTAAAGCGCCTTGAGAGACTCGGGCATTGGCTTT	385		
QY	460	GGAGCGCAACGCMATANTATGCGCGCGGAGCGGGAATTTGTTGTTGTGACAGACTCGGGGA	519		
DB	386	GGGGGAATATGMAATTTGAGGCGCTGA-TGGACGCTTATGTGTGCTACTACCACTGGTGA	444		
QY	520	CNATGATCCCGTAATCTCGCCCGGGGAACACTTAATACCCGCTGTCCTCANGAAGT	579		
DB	445	TGATGAT-CCCTGTCAACCCCAAGCTGGCACTGCGCCCATGCTGTATCC---AGGAT	499		
QY	580	GCACCCCTCTGGAGATCCCTTTAAACNCMNANTGAATATCTCNCNANGAAGAACTCMT	639		
DB	500	GCTCTCTCTGAGATTTGTTTCACAGCAGACATGATGATACACT-GAAGCAGAGCTCAT	558		
QY	640	TATGACACGCTTTAANCAATCGATGACNCGTGTCTCTGCACATTCACATGAGCGC	699		

DB	559	CATGACAGCTTCAAAACAATTGATGGGCCCGGGGTGAATTCGCACANTGCTAATGGAGC	618
OY	700	CTGCTACACANCAATTTCTTCCTCCCAACACTCTTCTTCNTNGCCTCCCTCC	752
Db	619	ATGCATCACCGCTCCAATTTGTCAGAGAATGTTATAATCATGCTGTCCATCC	671
RESULT 10			
LOCUS	B1959076	632 bp	mRNA linear EST 22-OCT-2001
DEFINITION	HVSMEN0018A17f Hordeum vulgare rachis EST library HVCDDNA0015		
ACCESSION	(normal) B1959076		
VERSION	B1959076.1		
KEYWORDS	GI:16310331		
SOURCE	EST.		
ORGANISM	Hordeum vulgare.		
REFERENCE	Hordeum vulgare.		
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum. 1 (bases 1 to 632) Wing R., Close T.J., Kleinhofs A., Wise R., Chin A., Begum D., Frisch D., Atkins M., Yu X., Henry D., Palmer M., Rambo T., Simmons , J., Gates R. and Main D. 'Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library Unpublished (2001) Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel.: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Total hg bases = 473 Seg primer: AATTACCCTCAGCTTAACGG High quality sequence stop: 613. Location/Qualifiers 1..632 /organism="Hordeum vulgare" /cultivar="Morex" /db_xref="taxon:4513" /clone="HVSMEN0018A17f" /clone_1fb="Hordeum vulgare rachis EST library HVCDDNA0015 (normal)" /tissue_type="Rachis" /lab_host="TJC121" /note="Vector: plunscript SK(-); Site.1: EcoRI; Site.2: XhoI; Plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give plunscript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of paired value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley . To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/g9pages/bgn/31/clover.html)"		
BASE COUNT	125 a	246 c	171 g 89 t others
ORIGIN			

Query Match	18.6%	Score 150	DB 13	Length 632
Best Local Similarity	67.2%	Pred. No. 4e-34		
Matches 254	Conservative 0	Mismatches 117	Indels 7	Gaps 4
QY	376	GGCAACCCGATGAGAGACTGCTGGCGGCGTGCGACCCCTGATTGTGACATGTCAACGAAAAAG	435	
Db	11	GGGAAACCCCATTCGAGAGACTGCTGGCGGCTTGCGACTGTGACACAAACCGGAGCGC	70	
QY	436	CTCGCTGACTGCGGATTTGGCTTTTGGAGCGCAACGCGNATANGTGGCCCGGAGGGAATTT	495	
Db	71	CTCGCGGACTCGGGATTCGGCTTGGCGCGCAACGCGCATCGCGCGCGGAC-GGGCAAT	129	
QY	496	GTTCGTTTGACAGACTCCGGGGGAGANATGATCCCGTGAATCCCTGCGCGGGAGACATT	555	
Db	130	CTAGTGTGTACCGAGCGGGGGAGAGAGACCCGGGAGAGACCCCAAGAAAGGACACCTTGC	189	
QY	556	NATACCCCGCTCTCCANGAAGTTGGCCCCCTCTGTGGATCCCTTTTAAACNCAANTTGA	615	
Db	190	GCTACGGCGGTATCC---AGGACGAGCGCGGTGTGATCATCTTCAACGCGACATATGTTC	245	
QY	616	ATTCNCTCNANGGAAGACTNTTATGAACAGTTTAAACNATGATGAGCNANGT	675	
Db	246	ATTCACCTTC-AGCCAGAGCTCATCATATAACAGCTTCAAGACATTCGACGCGCGGCGC	304	
QY	676	CCTGCTCAATTTGCCAATGGCGCCTGTCNCAACCAACCAATTTCTNTCCCAACNTCTCT	735	
Db	305	CAAGGTGACATTCGCGCAACGGCGCTCGACACCATTC-AGTACGTCAACCAAGTCATCA	363	
QY	736	TCGCTNCTGCTCCNCCGCC	753	
Db	364	TCACGGCTTCACATCC	381	

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RESULT 11
AV822011
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
Source

AV822011 679 bp mRNA EST 01-APR-2002
AV822011 RAFL4 Arabidopsis thaliana CDNA clone RAFL04-19-NO9 5',
mRNA sequence.
AV822011
AV822011.1 GI:19864043
EST.
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots:
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 679)
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
and Shinozaki,K.
Large scale analysis of Arabidopsis full-length CDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: meaki@rc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a SalI/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/Plant/index\_e.html) for
further details.
Location/Qualifiers
1..679
/organism="Arabidopsis thaliana"
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/clone_lib="RAFL4"
/dev_stage="rosette plants"

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/lab_host="SOLR"
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Best Local Similarity 65.3%; Pred. No. 6,3e-34;
Matches 269; Conservative 0; Mismatches 136; Indels 7; Gaps 4

OY 274 GAAGCCGAGTGTGACGACCCGAGAGAGTTGCTTGACGGTCTTATGACCAATTAATCAAC 333
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 275 GAACATGAGAGTTGAGAACACCCAGANTAAATCGCTGCGCATGTGGACATGAGATTGGAAC 334
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 334 AGCAGCGGTCCGAGATCTCTTGTTATCTGTCGTGCGGTGACGAGACCCGATGACGAC 393
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 335 AGCAGAGAGCGGAGAGAAAGATTAGGTTACTTCTCTCTCGCCACCGGACACCAATGCACAT 394
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 394 TGCTGGCGGTGCGACCTCGATTGGCATGTCAACAAAAAGCTCGTGCATGCGGCATT 453
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 395 TGCTGGCGGTGCGACCGCAAAATGGCAGCTCGCTCCCAACGTTTAGCCGATTGCTCAATC 454
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 454 GGCCTTGGACGCAACGCNATANGTGGCGGACGGGGAATTTGTTGCTTGACAGACTC 513
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 455 GGATTTCGCCGACAGCAATGGAAGGCGCGAC -GGTGTTCATGAGTGTGACCGACCC 513
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 514 TGGACAGACAGCAT -CCGTTAATCCATACGCGGAGAACATCGTCGACGCCGTGATT-C--- 569
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 574 GAAGTGGCCCCCTCTGGGATCCCTTTAAACNCAANTGGAATTCNCTGANGAAGA 633
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 570 -AAGACGAACCACTGTGATCATCTTCAACGCGCATGTTATTAAC -CTTGAACCAAGA 627
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 634 ACTCTTTATGAACACGCTTTAANACNATGATGAGACNCGTGTCTCTGCAC 685
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 628 GCTGATCATGAACAGACTTCAAAACCATGAGGTGTGTGTCATGTTTAC 679
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RESULT 12
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LOCUS BE035831
DEFINITION MO10G11 MO Mesembryanthemum crystallinum cDNA 5' similar to pectate
ACCESSION BE035831
VERSION BE035831.1 GI:8330840
KEYWORDS EST.
SOURCE Common Iceplant.
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eumariophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllales; Alzaceae; Mesembryanthemum;
1 (bases 1 to 883)
Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferreira,
H., Kawasak, S., McColough, A., Michalowski, C.B., Palacio, C.,
Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: chm@u.arizona.edu
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Location/Qualifiers
1..883
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/db_xref="taxon:3544"
/clone_lib="MO"
/tissue_type="apical meristem and leaf primordia"
/dev_stage="5 weeks"

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BASE COUNT	217 a	201 c	221 g	241 t	3 others
Query Match	18.5%	Score 149.2;	DB 10;	Length 883;	
Best Local Similarity	61.0%;	Pred. No. 8.3e-34;			
Matches 289;	Conservative 0;	Mismatches 177;	Indels 8;	Gaps 4;	
OR	280	GCACGTCACGACACCCGAGGAGTTCCTTCGACGGTCCTGATGACCATATATCAACGACAC	339		
DB	274	GCTGGGTGACACCCGAAAGAGGTCTTTTCCATGGTGACATGATGATGAGGAACGACTCT	333		
OR	340	GCTCGCAGATCTCTGTTATCTGTCTGTCGTCGCGGTTTCAGGCAACCCGATCGACGACTGTGG	399		
DB	334	CAGAGAGAGGAAGCTGGTGTATTCTTCATGTCGGAGACGGAATTCATATGATGATGTCGG	393		
OR	400	CGGTGCGACCTGATTTGGCATGTCAACGAAAAAAGTCCTGACTGCGGCATTGGCTTT	459		
DB	394	CGTGTGTATCCCAACTGGCACAAAAACCGCAAGCGCCTAGCTGATGTGTGTGATTTGGCTTT	453		
OR	460	GGACGCAACGCAATATGATGTCGCGGAGGGGAATTTGTTCTGTTGACAGACTCCGGGGA	519		
DB	454	GGACAAATTCCTCATTTGTGTGCGCG -GAACGGTCGCTTATGTTGTCACAGACTGTGGTGA	512		
OR	520	CNATGATCCCGTGAATCCTCGCGCGGAGACACTTANATACCCGCTTCACANCAAGATT	579		
DB	513	TGATGAT -GCTGTCAACCTTAAGCCTGCGACACTCTTCTGTCATGACATCATCAGAA ---	567		
OR	580	GCCCCCTGGGATCCCTTTAAACNCNAATNGAAATCTCNCNCNANGAAGAACTCT	639		
DB	568	-GAGCTCTGTGATCGTTTTCAGCGCTGACATGATGTATCCAGTTGAAGCAGGACTTAT	626		
OR	640	TATGAACAGCTTTTANACNATGATGACGNCNGTGTCCCTGCTCCACATTTGCCAATGGCGC	699		
DB	627	AATGAACAGCTTCAAGACAAATGATGAGCGCGTGATCTATATGTCCACATAGTAATGAGAC	686		
OR	700	CTGCTACCCANCAATTTCTTCCCAACATCTTCTTCCATNGCTCCNCTGCC	753		
DB	687	TTGCAATCAATTCATATTT -GTGACAAACATCATATTCACGCGCATTCACATTC	739		
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LOCUS	B0148154	612 bp	mRNA	linear	EST 24-Apr-2002
DEFINITION	NP062C07FL1P1054	Developing flower	Medicago truncatula	cdna clone	
ACCESSION	B0148154				
VERSION	B0148154.1	GI:20285213			
KEYWORDS	EST.				
SOURCE	barrel medic.				
ORGANISM	Medicago truncatula				
REFERENCE	Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,				
AUTHORS	Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.				
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation				
JOURNAL	Medicago truncatula flower library				
COMMENT	Unpublished (2001)				
FEATURES	Plant Biology Division				
source	The Samuel Roberts Noble Foundation				
	2510 Sam Noble Parkway, Ardmore, OK 73402, USA				
	Tel: 580 221 7391				
	Fax: 580 221 7380				
	Email: gdmay@noble.org				
	Insert length: 612 Std Error: 0.00				
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QY 711 NCCATTT 717
DB 414 TTCAGTT 420

RESULT 15
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LOCUS fc2443.e Rose Petals (Fragrant Cloud) Lambda Zap Express Library
DEFINITION Rosa hybrid cultivar cDNA clone fc2443.e 5', mRNA sequence.
ACCESSION BO104182
VERSION BO104182.1 GI:20153844
KEYWORDS EST.
SOURCE Rosa hybrid cultivar.
ORGANISM Rosa hybrid cultivar.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosid I; Rosales; Rosaceae; Rosoideae; Rosa.
1 (bases 1 to 518)
Menda, N., Guterman, I., Plestun, D., Emanuel, M., Adam, Z., Pichersky
, E., Lewinsohn, E., Zamir, D., Vainstein, A. and Weis, D.
Rosa petal genomics: an integrated approach to discover
fragrance-related genes
Unpublished (2002)
Contact: Naama Menda
Petal Genomics
Faculty of Agricultural, Food and Environmental Quality Sciences,
The Hebrew University of Jerusalem
P.O. Box 12, Rehovot, 76100, Israel
Tel: 972 8 9489 389
Fax: 972 8 9468 263
Email: shahamagrl.huji.ac.il
Seq primer: T3 forward.
Location/Qualifiers
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/strain="Fragrant Cloud"
/db_xref="taxon:128735"
/clone="fc2443.e"
/clone_1lb="Rose Petals (Fragrant Cloud) Lambda Zap
Express Library"
/tissue-type="Petals"
/dev_stage="Young open flower at stage four"
/Note="Vector: pBKCMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 134 a 129 c 147 g 108 t
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Query Match 17 5%; Score 141.2; DB 14; Length 518;
Best Local Similarity 63.1%; Pred. No. 1.7e-31;
Matches 268; Conservative 0; Mismatches 150; Indels 7; Gaps 4;
QY 274 GAAGCCGAGTCGACGACCCGAGAGGTTGCTTCAGTCGTCCTGATGACCATATCAAC 333
DB 99 GAGCAGCGAGTGAATATTCGAGAGATCCGCTCTGTTGATGACACCATTTGTAAC 158
QY 334 AGCAGGGCTCGCAGATCTCTGTTATCTGTCTGTCGGGTTGAGCAACCGATCGACGAC 393
DB 159 AGTACTGCGAGAGAACTTGGGATTTTTCATGTCGCAACAGGGAATCCCATTTGATGAC 218
QY 394 TGTGGGCGTGGACCTGATTTGGCATGTCAACAGAAAAAGCTTGGTACTGGCGATT 453

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DB 219 TCCTGAGATGTGACCCACAAATGCGACGCCACCCAGAGAGCTAGCCAACTGCGGCAATT 278
QY 454 GGCTTTGAGACGACGACNATANGTGCCGCGGAGGGAATTTGTTGTTGACAGATC 513
DB 279 GGGTTTGGCGGACAGCTGTGCGGCGGCTTGAC-GGAGGTACTACGTGTAAATGACCC 337
QY 514 CGGGGACNATGATCCCGGTAATCCTCGCCCGGGAACACTTANATACCCGTCNTCCAA 573
DB 338 CGGTGATGATGA-CCGGGTGAACCCCGGCGGTAACTCCGTCCGTCACGCTGTCATTCAGG 396
QY 574 GAAGTTGCCCTCTGGGATCCCTTTAANACNMANATGGAATCTCNCNTCANGAAGA 633
DB 397 ACAG---GCTTTGTGATGTGTCAAGCGGTGACATGTGATCACA-TTGAACGACGA 451
QY 634 ACTGTTATGAACAGCTTTAANACNATGAGACNCGTGTCTGTCACATTCGCA 693
DB 452 GCTTATATGAACAGCTTCAAGACCATTTGACGCTGTGAGTCAATGTTCACATTTCTTA 511
QY 694 TGGCG 698
DB 512 TGGAG 516

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Job time : 1456 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 00:40:52; Search time 68 Seconds
(without alignments)
3635.022 Million cell updates/sec

Title: US-09-966-881-13

Perfect score: 806

Sequence: 1 TGTTCCTCCTTCGATCACA.....TCCCTTCCTCATGATGATG 806

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	55.6	6.9	1170	3 US-08-467-023-94	Sequence 94, Appl
2	55.2	6.8	1337	3 US-08-467-023-96	Sequence 96, Appl
3	55.4	6.7	1278	3 US-08-467-023-96	Sequence 96, Appl
4	46.6	5.8	1328	1 US-08-290-448A-58	Sequence 58, Appl
5	46.6	5.8	1328	1 US-08-290-448A-58	Sequence 58, Appl
6	46.6	5.8	1328	1 US-08-175-069A-58	Sequence 58, Appl
7	46.6	5.8	1328	1 US-08-175-069A-58	Sequence 58, Appl
8	46.6	5.8	1328	4 US-08-461-939B-58	Sequence 58, Appl
9	46.6	5.8	1349	1 US-08-464-000-58	Sequence 58, Appl
10	46.6	5.8	1349	1 US-08-280-448A-73	Sequence 73, Appl
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18	43.8	5.4	1320	4 US-08-461-939B-75	Sequence 75, Appl
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23	41.8	5.2	1160	4 US-08-461-939B-77	Sequence 77, Appl
24	41.8	5.2	1160	4 US-08-464-000-77	Sequence 77, Appl
25	38.8	4.8	1196	1 US-08-280-448A-71	Sequence 71, Appl
26	38.8	4.8	1196	1 US-08-290-448A-71	Sequence 71, Appl
27	38.8	4.8	1196	1 US-08-175-069A-71	Sequence 71, Appl

28	38.8	4.8	1196	4 US-08-461-939B-71	Sequence 71, Appl
29	38.8	4.8	1196	4 US-08-464-000-71	Sequence 71, Appl
30	36.6	4.5	1036	4 US-09-072-596-304	Sequence 304, App
31	35.2	4.4	1368	1 US-08-290-448A-79	Sequence 79, Appl
32	35.2	4.4	1368	1 US-08-290-448A-79	Sequence 79, Appl
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37	34	4.2	4411529	4 US-09-103-840A-1	Sequence 1, Appl1
38	33.6	4.2	7218	1 US-08-282-463-14	Sequence 14, Appl
39	33	4.1	726	4 US-08-818-112-24	Sequence 24, Appl
40	33	4.1	726	4 US-08-818-111-24	Sequence 24, Appl
41	33	4.1	726	4 US-09-056-556-24	Sequence 24, Appl
42	33	4.1	726	4 US-09-072-596-24	Sequence 24, Appl
43	33	4.1	33529	4 US-09-144-085-3	Sequence 3, Appl1
44	33	4.1	4403765	4 US-09-103-840A-2	Sequence 2, Appl1
45	33	4.1	4411529	4 US-09-103-840A-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-467-023-94
Sequence 94, Application US/08467023
Patent No. 6090386
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Bruner, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 1170 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE: CDS
NAME/KEY: 26..1126
LOCATION: 26..1126
FEATURE: mat.peptide
NAME/KEY: 89..1126
LOCATION: 89..1126
US-08-467-023-94

Query Match 6.9%; Score 55.6; DB 3; Length 1170;
Best Local Similarity 62.5%; Pred. No. 2.7e-07;
Matches 85; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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DB 73 TGTATCTGTTACTGTGATTAATCCATCGACAGCTGCTGGAGGATTCGAACTGGCA 132
QY 420 TCTCAACAGAAAAAGCTGCTGATGCGGCAATGGCTTGGACGCAACGNAATANGTG 479
DB 133 TCMAAACGAAATGAAAGCTGCGAGACTGTCTGTGGGATTGGAAAGCTCCACCAATGGGAGG 192
QY 480 CCGGACGGGGAATTT 495
DB 193 CAAGAGAGAGATTTT 208

RESULT 2
US-08-467-023-1
Sequence 1, Application US/08467023
Patent No. 6090386

GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
NUMBER OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1337 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Crypthomeria japonica
FEATURE:
NAME/KEY: CDS
LOCATION: 66..1187
FEATURE:
NAME/KEY: mat.peptide
LOCATION: 129..1187
US-08-467-023-1

Query Match 6.8%; Score 55.2; DB 3; Length 1337;
Best Local Similarity 51.7%; Pred. No. 3.8e-07;
Matches 181; Conservative 0; Mismatches 159; Indels 10; Gaps 3;

QY 349 TCTCTGTTATCTCTGTCGTCGCTTACGACACCCGATGACGACGTCGTCGGGTCGAC 408
DB 102 TCTTTTGTATGATGATCTGCTTCTGTATATCCCATGACAGCTGCTGCGAGAGAGAC 161
QY 409 CCTGATGGCATGTCACAGAAAAAGCTGCTGACGCGGATGCGCTTTGAGCGAAC 468
DB 162 TCAAACTGGGCCCCAAATGATGAACTCGACAGATTGTCAGTGGCTTGGAGACTCC 221
QY 469 GCNATANGTGCCGCGACGGGGAATTTGTTCTGTGACAGACTCGGGGACNATGATCC 528
DB 222 ACCATGGGAGGAGGAGAGAG-ATCTTATACGGTCAAGACTCAGATGACGA-----CC 276
QY 529 CCGTGAATCCGCCCCGGAACACTTANATCCCGCTGTCNAAAGAGTTGCCCTCT 588
DB 277 CTGTAAATCTGACACGAGAACTGCGCTATGAGCAACCGGATAGGCCCTGTGGA 336
QY 589 GGGATCCCTTAAACNCAANTGGAATCTCTCNCNANGAAGAACTCNTATGAGACG 648
DB 337 TAATTTGAGTGGGAATGAAATATAAGCTCAAAATGOCATATGAC-----ATTGCTGG 391
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DB 392 GTATAAGACTTTGATGCGAGGGAGCAAGTTATATATGCAATGGCG 441

RESULT 3
US-08-467-023-96
Sequence 96, Application US/08467023
Patent No. 6090386

GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.;
APPLICANT: Pollock, Joanne;
APPLICANT: Bond, Julian F.;
APPLICANT: Garman, Richard D;
APPLICANT: Kuo, Mei-Chang;
APPLICANT: Yeung, Siu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
NUMBER OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 1278 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 36..1145
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 99..1145
US-08-467-023-96

Query Match 6.7%; Score 54; DB 3; Length 1278;
Best Local Similarity 61.8%; Pred. No. 8.6e-07;

Matches 84; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 360 TCTTCCTGCGTTCAGCAACCCGATCGACGACTGCTGGCGGTGCGACCTGATTTGCA 419
DB 83 TGTATCTGTGCTCTATATATCCATAGACGCTGCTGAGAGAGATTGCACTGGG 142
QY 420 TGTCAAGAAAAAGCTCGCTGACTGCGGCGATTGGCTTGACGCAACGCGNATANGTG 479
DB 143 TCAAAACAGATGAAGCTCGAGATTGCGCTGTGGATTGGAAGCTCCACCATGGAGG 202
QY 480 CCGCGACGGGGAATTT 495
DB 203 CAAGGAGAGATTTT 218

RESULT 4

US-08-290-448A-58
Sequence 58, Application US/08290448A
Patent No. 5676954
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,448A
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365

FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 1328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1328
US-08-290-448A-58

Query Match 5.8%; Score 46.6; DB 1; Length 1328;
Best Local Similarity 46.7%; Pred. No. 0.00016;

Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGTGGGTTTCAGCAACCCGATCGACGACTGCTGGCGGCGGACCTGATTTGCA 424
DB 113 CATGTGAAGCACACACATATAGACAAGTCTGAGGTGCAAGCGATTTGGCGAATA 172
QY 425 ACAGAAAAAGCTGCTGACGCTGCGGCAATGGCTTTGACGCAACGCGNATANGTGCGCGG 484
DB 173 ACCGACAAGCGTTGACCGGATTTGCCCAAGGTTTGGCAAGGAACCTACGCGGAAAC 232
QY 485 ACGGGGAATTTGCTGTGTGACAGACTCCGGGGACNATGATCCCGGATTCCTCGCC 544
DB 233 ATGTGAT-----GCTACACGGTACCGAGTATAAGTATGATGTTGCAAAATCCA 285
QY 545 GGAACACTANATACCCGCTGCTCCCAANGAAGTTGCCCTCTGGGATCCCTTTAAAC 604
DB 286 AAGAGGACACACTCCGGTTGCTGTCGCCAANAAGCCCTTGTGATCATTTTAA 345
QY 605 NCNANTGGAATCTCNCCTCANGAAGAACTCTTTATGAACACTTTAANACATGAT 664
DB 346 AGAATATGATGATTCATTTGAATCAAGAGCTTGTGTAACACGCAAGACCATCAT 405
QY 665 GGACNCNGTCTCTGTCACATTTGCCAATGGCG 698
DB 406 GGCCGAGGGGTGAAGTATACATGTTAAGCCG 439

RESULT 5

US-08-290-448A-58
Sequence 58, Application US/08290448A
Patent No. 5698204
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/290,448A
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 1328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1328
US-08-290-448A-58

Query Match 5.8%; Score 46.6; DB 1; Length 1328;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CCGCGGTTCCAGCAACCCGATGACGACTGCTGGCGGCGCACTTGGCATGTCA 424
DB 113 CATGTGAGACACACACATTAATAGACAACTGCTGGAGGTGCAAAAGCGATGGCGAATA 172
QY 425 ACAGAAAAAGCTCGCTGACTCGGCAATGGCTTGGACGCAACGCMATANGTGCCGCG 484
DB 173 ACCGACAAACGCTTAGCCGATGTGGCCCAAGTTTCCAAAGGAACCTACGCTGGAAGAAC 232
QY 485 ACGGGGAATTTGTTGCTGTGACAGACTCCGGGGACMATGATCCCGGATTCCTGCGCC 544
DB 233 ATGGTGAT-----GTCTACACGGTCAACAGTGAATAAGATGATGTGCAATCA 285
QY 545 GGGAACTTANATACCCGCTCCTCCCAANGAGTGGCCCTCTGGGATCCCTTTAAAC 604
DB 286 AAAGAAGGACACACTCGGTTGCTGCTGCCAAACAGGCCCTTGATGATTTTAA 345
QY 605 NCNANTGGAATCTCNCNANGAAGAACTTTATGACAGCTTTAANCMATCGAT 664
DB 346 AAAAAATATGATTCATTGATTAATCAAGAGCTTGTGTAACAGGACAGACATCAT 405
QY 665 GGACNCGTGTCTGTCACATTCGCAATGGCG 698
DB 406 GGCCGAGGGGTGAAGTTAACTGTTAAAGCGCG 439

RESULT 6
US-08-175-069A-58
Sequence 58, Application US/08175069A
Patent No. 5776761
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rainier, Thorun
APPLICANT: Kuo, Mel-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,069A
FILING DATE: December 29, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 1328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1328
US-08-175-069A-58

Query Match 5.8%; Score 46.6; DB 1; Length 1328;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CCGCGGTTCCAGCAACCCGATGACGACTGCTGGCGGCGCACTTGGCATGTCA 424
DB 113 CATGTGAGACACACACATTAATAGACAACTGCTGGAGGTGCAAAAGCGATGGCGAATA 172
QY 425 ACAGAAAAAGCTCGCTGACTCGGCAATGGCTTGGACGCAACGCMATANGTGCCGCG 484
DB 173 ACCGACAAACGCTTAGCCGATGTGGCCCAAGTTTCCAAAGGAACCTACGCTGGAAGAAC 232
QY 485 ACGGGGAATTTGTTGCTGTGACAGACTCCGGGGACMATGATCCCGGATTCCTGCGCC 544
DB 233 ATGGTGAT-----GTCTACACGGTCAACAGTGAATAAGATGATGTGCAATCA 285
QY 545 GGGAACTTANATACCCGCTCCTCCCAANGAGTGGCCCTCTGGGATCCCTTTAAAC 604
DB 286 AAAGAAGGACACACTCGGTTGCTGCTGCCAAACAGGCCCTTGATGATTTTAA 345
QY 605 NCNANTGGAATCTCNCNANGAAGAACTTTATGACAGCTTTAANCMATCGAT 664
DB 346 AAAAAATATGATTCATTGATTAATCAAGAGCTTGTGTAACAGGACAGACATCAT 405
QY 665 GGACNCGTGTCTGTCACATTCGCAATGGCG 698
DB 406 GGCCGAGGGGTGAAGTTAACTGTTAAAGCGCG 439

RESULT 7
US-08-461-939B-58
Sequence 58, Application US/08461939B
Patent No. 6335019
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rainier, Thorun
APPLICANT: Kuo, Mel-chang
TITLE OF INVENTION: Methods For Treating Sensitivity To A
TITLE OF INVENTION: Protein Allergen Using Peptides Which Include A T Cell Epit
NUMBER OF SEQUENCES: 93

Db 194 ACCGACAGCGTTAGCCGATTGTCGCCAAGTTTTGCCAAAGGAACCTACGGTGGAAAAC 253
QY 485 ACGGGGAATTTGTTGTTGTGACAGACTCCGGGGACNATGATCCCGTGATCCTCGCCC 544
Db 254 ATGGTGAAT-----GCTACACGGTCAACGATGATTAAGATGATGTTGCAAAATCCA 306
QY 545 GGGAACTTANATATACCCCGTCTCCACANGAAGTTGCCCTCTGGATCCCTTTAAAC 604
Db 307 AAAGAAAGCACACACCTCCGTTTGGCTGCTGCCAAAACAGGCCCTTGATGATCATTTTAAA 366
QY 605 NCNAAATGGAATATCTCTCNCNANGAAGAACTCTTTTGAACACTTTAANACNATGAT 664
Db 367 AGAAATATGTTGATTCATTGGAATCAAGACCTTGTGTTAAACAGCAGCAAGACCATGAT 426
QY 665 GGACNCNGTGTCTGTCACATTCACCATGCGC 698
Db 427 GGCCGAGGGGTGAAGTTAACTATGTTAAGCGCG 460

RESULT 11

US-08-175-069A-73
Sequence 73, Application US/08175069A
Patent No. 576761

GENERAL INFORMATION:

APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,069A
FILING DATE: December 29, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018DV
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1323
US-08-175-069A-73

Query Match 5.8%; Score 46.6; DB 1; Length 1349;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGTGGGTTAGGCAACCCGATCGACAGCTGCTGGCGGTGGAGACCTGATTTGCATGTCA 424
Db 134 CATGTGAAGACACACATATTATAGCAAGTCTGTGAGTGTGAAGCCGATTTGGCGATA 193
QY 425 ACAGAAAAAAGCTGCTGACTGCGGCAATTGGCTTTGAGACGACNATANGTGGCCGC 484
Db 194 ACCGACAGGTTAGCCGATTTGTCGCCAAGGTTTGCAAAGGAACCTACGGTGGAAAAC 253
QY 485 ACGGGGAATTTGTTGTTGTGACAGACTCCGGGGACNATGATCCCGTGATCCTCGCCC 544
Db 254 ATGGTGAAT-----GCTACACGGTCAACGATGATTAAGATGATGTTGCAAAATCCA 306
QY 545 GGGAACTTANATATACCCCGTCTCCACANGAAGTTGCCCTCTGGATCCCTTTAAAC 604
Db 307 AAAGAAAGCACACCTCCGTTTGGCTGCTGCCAAAACAGGCCCTTGATGATCATTTTAAA 366
QY 605 NCNAAATGGAATATCTCTCNCNANGAAGAACTCTTTTGAACACTTTAANACNATGAT 664
Db 367 AGAAATATGTTGATTCATTGGAATCAAGACCTTGTGTTAAACAGCAGCAAGACCATGAT 426
QY 665 GGACNCNGTGTCTGTCACATTCACCATGCGC 698
Db 427 GGCCGAGGGGTGAAGTTAACTATGTTAAGCGCG 460

RESULT 12

US-08-461-939B-73
Sequence 73, Application US/08461939B
Patent No. 6335019

GENERAL INFORMATION:

APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Methods For Treating Sensitivity To A
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,939B
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/464,000
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/290,448
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CNDV
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1323
US-08-461-939B-73

Query Match 5.8%; Score 46.6; DB 4; Length 1349;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGTGGCGTTACGCAACCCGATCGAGCTGCTGGCGGTGCGACCCCTGATGGCATGTCA 424
DB 134 CATGTGAACACACACATTATAGACAACTGCTGGAGGTGCAAGCCGATGGCGGAATA 193
QY 425 ACAGAAAAAGCTCGCTGACTCGGCGATGCTTGGACGCAACGCNATANGTGGCCGG 484
DB 194 ACCGACAAACGTTAGCCGATTTGCCCAAGGTTTGCACAAAGGAACCTACGGTGGAAAC 253
QY 485 ACGGGGAATTTGTTGTTGTGACAGACTCGGGGACNATGATCCCGGTAATCTCGCCC 544
DB 254 ATGGTGAT-----GTCTACACGGTCAACAGTGAATAAGATGATGTGCAATCCA 306
QY 545 GGAACACTTANATACCCCGTCCNTCCANAGATTGCCCTCTGGGATCCCTTAAAC 604
DB 307 AAGAAGGACACACTCCGTTTCTGCTGCCCAAAACAGCCCTTGTGATCATTTTAA 366
QY 605 NCNAAATGGAATCTCNCNCNANGAAGAACTNTATGACAGCTTTAANACNATCAT 664
DB 367 ACAAATATGTTGATTCATTGTAATCAAGAGCTTGTGTAACAGGACAGACATCATCAT 426
QY 665 GCACNCGTGTCTCTGTCACATTCGCAATGGCG 698
DB 427 GGCCGAGGGGTGAAGTTAACAATCGTTAAGCCG 460

RESULT 13
US-08-464-000-73

; Sequence 73, Application US/08464000
; Patent No. 6335020

; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce
; APPLICANT: Klapper, David G.
; APPLICANT: Rafnar, Thorunn
; APPLICANT: Kuo, Mel-Chang
; TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,000
; FILING DATE: 05-JUN-1995

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/290,448
; FILING DATE: 15-AUG-1994
; APPLICATION NUMBER: US 07/529,951
; FILING DATE: 29-MAY-1990
; APPLICATION NUMBER: US 07/325,365
; FILING DATE: 17-MAR-1989

; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-018CN2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1323
US-08-464-000-73

Query Match 5.8%; Score 46.6; DB 4; Length 1349;
Best Local Similarity 46.7%; Pred. No. 0.00016;
Matches 156; Conservative 0; Mismatches 171; Indels 7; Gaps 1;

QY 365 CGTGGCGTTACGCAACCCGATCGAGCTGCTGGCGGTGCGACCCCTGATGGCATGTCA 424
DB 134 CATGTGAACACACACATTATAGACAACTGCTGGAGGTGCAAGCCGATGGCGGAATA 193
QY 425 ACAGAAAAAGCTCGCTGACTCGGCGATGCTTGGACGCAACGCNATANGTGGCCGG 484
DB 194 ACCGACAAACGTTAGCCGATTTGCCCAAGGTTTGCACAAAGGAACCTACGGTGGAAAC 253
QY 485 ACGGGGAATTTGTTGTTGTGACAGACTCGGGGACNATGATCCCGGTAATCTCGCCC 544
DB 254 ATGGTGAT-----GTCTACACGGTCAACAGTGAATAAGATGATGTGCAATCCA 306
QY 545 GGAACACTTANATACCCCGTCCNTCCANAGATTGCCCTCTGGGATCCCTTAAAC 604
DB 307 AAGAAGGACACACTCCGTTTCTGCTGCCCAAAACAGCCCTTGTGATCATTTTAA 366
QY 605 NCNAAATGGAATCTCNCNCNANGAAGAACTNTATGACAGCTTTAANACNATCAT 664
DB 367 ACAAATATGTTGATTCATTGTAATCAAGAGCTTGTGTAACAGGACAGACATCATCAT 426
QY 665 GCACNCGTGTCTCTGTCACATTCGCAATGGCG 698
DB 427 GGCCGAGGGGTGAAGTTAACAATCGTTAAGCCG 460

RESULT 14
US-08-232-463-14

; Sequence 14, Application US/08232463
; Patent No. 5670367

; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE: 05-07-935,313

; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-018CN2

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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 00:46:15 ; Search time 166 Seconds
(without alignments)
7124.978 Million cell updates/sec

Title: US-09-966-881-13

Perfect score: 806
Sequence: 1 TGTTCCTCCTCGATCACA.....TCCCTTCCTCTATGATNG 806

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0

Maximum DB seq length: 200000000

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Maximum Match 100%

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Published Applications_NA: *
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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	134.6	16.7	687	10	US-09-966-881-14
6	124.2	15.4	1116	9	US-09-938-842A-1004
7	110.4	13.7	1215	9	US-09-938-842A-58
8	93.4	11.6	460	10	US-09-770-444-439
9	93	11.5	479	10	US-09-924-035A-174
10	74.4	9.2	1629	9	US-09-938-842A-1766
11	68.4	8.5	277	10	US-09-923-876-4484
12	64.4	8.0	1185	9	US-09-938-842A-809
13	56.2	7.0	388	10	US-09-878-574-3663
14	43.6	5.4	741	10	US-09-966-881-15
15	41	5.1	1137	10	US-09-828-505-3
16	37.6	4.7	481	9	US-09-918-995-25
17	37.4	4.6	708	9	US-10-123-155-298
18	35.6	4.4	360	10	US-09-864-761-27334
19	35.6	4.4	496	10	US-09-864-761-10689

20	35.2	4.4	594	9	US-10-123-155-10	Sequence 10, Appl
21	35.2	4.4	15425	9	US-10-091-504-1654	Sequence 1654, Ap
22	35.2	4.4	15425	10	US-09-764-869-1654	Sequence 1654, Ap
23	34.8	4.3	451	9	US-10-123-155-126	Sequence 126, Appl
24	34.4	4.3	1732	10	US-09-789-561-21	Sequence 29, Appl
25	34.2	4.2	4100	9	US-09-373-658-29	Sequence 96, Appl
26	34	4.2	2396	9	US-10-098-841-96	Sequence 97, Appl
27	34	4.2	2663	9	US-10-098-841-97	Sequence 5756, Ap
28	34	4.2	4332	9	US-09-764-891-5756	Sequence 10, Appl
29	34	4.2	7149	9	US-10-166-935A-1	Sequence 10, Appl
30	34	4.2	14155	9	US-10-108-605-102	Sequence 60, Appl
31	33.8	4.2	724	9	US-10-123-155-60	Sequence 346, Appl
32	33.8	4.2	1049	9	US-10-123-155-358	Sequence 4, Appl
33	33.4	4.1	437	10	US-09-960-352-12835	Sequence 210, Appl
34	33.4	4.1	671	9	US-10-184-644-346	Sequence 1, Appl
35	33.4	4.1	671	9	US-10-184-644-346	Sequence 34, Appl
36	33.4	4.1	2380	9	US-09-964-992A-4	Sequence 346, Appl
37	33.2	4.1	407	10	US-09-878-574-4048	Sequence 4, Appl
38	33	4.1	519	9	US-10-123-155-210	Sequence 4048, Ap
39	32.8	4.1	638	9	US-10-013-173-1	Sequence 210, Appl
40	32.8	4.1	638	9	US-10-150-762-1	Sequence 1, Appl
41	32.8	4.1	661	9	US-10-121-988-34	Sequence 34, Appl
42	32.8	4.1	661	10	US-09-884-998-34	Sequence 34, Appl
43	32.8	4.1	1064	10	US-09-804-682-29	Sequence 34, Appl
44	32.8	4.1	2481	9	US-10-121-988-35	Sequence 29, Appl
45	32.8	4.1	2481	10	US-09-894-998-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-09-966-881-13
Sequence 13, Application US/09966881
Patent No. US20020120960A1
GENERAL INFORMATION:
APPLICANT: Seymour, Graham
Bird, Colin
TITLE OF INVENTION: Genetic control of Fruit Ripening
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zeneca Ag Products Inc.
STREET: 1800 Concord Pike
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/966, 881
FILING DATE: 28-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/242, 860
FILING DATE: 29-Mar-1999
APPLICATION NUMBER: GB 9618862.8
FILING DATE: 10-Sep-1996
APPLICATION NUMBER: GB 9708366.1
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: PCT/GB97/02424
FILING DATE: 08-Sep-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschultz, Ilya D.
REGISTRATION NUMBER: 33, 712
REFERENCE/DOCKET NUMBER: SEE 50183/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 13:


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Db      ||||| 248 CTTGGAGAGAGGGCTGTACACGAGGAGAGAGCCGANTGAGAGACCCGAGAGG 307
QY      ||||| 302 TTGCTTGAGAGGTCCTGATGACATTAATCAACAGACAGGCTCGAGATCTTGTTATC 361
Db      ||||| 308 TTGCTTGAGAGGTCCTGATGACATTAATCAACAGACAGGCTCGAGATCTTGTTATC 367
QY      ||||| 362 TGTGCTGCTGTCAGGACACCCGATGACAGACTGCTGGCGTGGCAGCTGATGGCATG 421
Db      ||||| 368 TGTGCTGCTGTCAGGACACCCGATGACAGACTGCTGGCGTGGCAGCTGATGGCATG 427
QY      ||||| 422 TCAACAGAAAAAGCTGCTGATGCGGACATGCTTGG-AGCAGACGATATGATGCGC 480
Db      ||||| 428 TCAACAGAAAAAGCTGCTGATGCGGACATGCTTGGCGCCCAACGCGATATGATGCGC 487
QY      ||||| 481 CGGAGCGGGAATTTGTTGTTGATGACAGACTCGGGGAGACATATGCGGATGATGCTC 540
Db      ||||| 488 CGGAGCGGGAATTTGTTGTTGATGACAGACTCGGGGAGACATATGATGCGGATGATGCTC 546
QY      ||||| 541 GCGCGGAGACACTTAATATACCCGCTGTCACANGAAGTTGCCCTGAGATCCCTTT 600
Db      ||||| 547 CCGCGGAGACACTTAATATATCCCGCTGATCCAG--ANCTNCCCTCTGATGATCCTTT 603
QY      ||||| 601 AACNCNANTGAAATCTCTCTNANGAAGAACTCTTATGAACAGCTTTAANACAT 660
Db      ||||| 604 AACACACATTTGAA-ATCNCGCCGAGAACTCTTNTAAGCCTTTNNAACATC 662
QY      ||||| 661 CGATGACNCGTCTGCTGTCACATTTGCCAATGGGCGCTGCTGACNCAATTCN 720
Db      ||||| 663 NATGACNCGTCTGCTGTCACATTTGCCAATGGGCGCTGCTGACNCAATTCN 722
QY      ||||| 721 TCCCC 725
Db      ||||| 723 TCNCC 727

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RESULT 3
 US-09-966-881-18
 ; Sequence 18, Application US/09966881
 ; Patent No. US20020120960A1
 ; GENERAL INFORMATION:

APPLICANT: Seymour, Graham
 Bird, Colin
 Medina-Suarez, Rosybel
 TITLE OF INVENTION: Genetic control of Fruit Ripening
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Zeneca Ag Products Inc.
 STREET: 1800 Concord Pike
 CITY: Wilmington
 STATE: DE
 COUNTRY: USA
 ZIP: 19850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/966,881
 FILING DATE: 28-Sep-2001
 CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/242,860
 FILING DATE: 29-Mar-1999
 APPLICATION NUMBER: GB 9618862.8
 FILING DATE: 10-Sep-1996
 APPLICATION NUMBER: GB 9708366.1
 FILING DATE: 25-Apr-1997
 APPLICATION NUMBER: PCT/GB97/02424
 FILING DATE: 08-Sep-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Hohenschutz, Liza D.

```

; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: SEE 50183/USP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 724 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: 0-0117
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-966-881-18

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Query Match 66.5%; Score 536; DB 10; Length 724;
 Best Local Similarity 89.7%; Pred. No. 2,9e-165;
 Matches 617; Conservative 0; Mismatches 62; Indels 9; Gaps 5;

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QY      6 TCTCCTTGATCATATCTTTTCTGCTGGAAGAGTGAGAGAGAGGCGCAAT 65
Db      9 TCTCCTTGATCATATCTTTTCTGCTGGAAGAGTGAGAGAGGCGCGCAAT 68
QY      66 GACGGCGGTTTAAAGATGATCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCT 125
Db      69 GACGGCGGTTTAAAGATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 128
QY      126 TTGAACGAGAGTGGGGGTGATTTGGAAGAGAGTCTCTGCTGAGAGATGGCG 185
Db      129 TTGAACGAGAGTGGGGGTGATTTGGAAGAGAGTCTCTGCTGAGAGATGGCG 188
QY      186 AGCATGCGGAGAGACTTTGAGAGAGGCTCCGCAACGACGACGACGCGATGCTCTT 245
Db      189 AGCATGCGGAGAGACTTTGAGAGAGGCTCCGCAACGACGACGCGATGCTCTT 248
QY      246 GAAAGAGAGGCTGTAAACCGGCGAGAGAAAGCCGACATGACGACCCGAGAGTTGC 305
Db      249 GAAAGAGAGGCTGTAAACCGGCGAGAGAAAGCCGACATGACGACCCGAGAGTTGC 308
QY      306 TTGACGCTCTGATGACATTAATCAACAGAGGCTGCGAGATCTTGTGTTATCTC 365
Db      309 TTGACGCTCTGATGACATTAATCAACAGAGGCTGCGAGATCTTGTGTTATCTC 368
QY      366 GTGCGGTCAGGCAACCCGATGACAGACTGCTGGCGGTGCAACCTGATTTGCAATCA 425
Db      369 GTGCGGTCAGGCAACCCGATGACAGACTGCTGGCGGTGCAACCTGATTTGCAATCA 428
QY      426 CAGAAAAAGCTGCTGACTCGGCGATTTGGACGCAACGCMATANGTGGCCGGA 485
Db      429 CAGAAAAAGCTGCTGACTCGGCGATTTGGACGCAACGCMATANGTGGCCGGA 488
QY      486 CGGGAATTTGTTGTTGATGACAGACTCGGGGAGCMATANGTGGCCGGA 545
Db      489 CGGGAATTTGTTGTTGATGACAGACTCGGGGAGCMATANGTGGCCGGA 547
QY      546 GGAACACTTANATACCCGCTGTCNCAANGAAGTGGCCCTCTGGGATCCCTTTAAACN 605
Db      548 GGAACACTTANAT-NCGGCTGTCNCAANGAAGTGGCCCTCTGGGATCCCTTTAAACN 603
QY      606 CNAANTGGAATCTGCTGTCNCAANGAAGTGGCCCTTTATGACAGC--TTTAAACNATGA 663
Db      604 C-ACNTGGAATCTGCTGTCNCAANGAAGTGGCCCTTTATGACAGC--TTTAAACNATGA 661
QY      664 TGACNCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 691
Db      662 NGACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 689

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RESULT 4
 US-09-966-881-17
 ; Sequence 17, Application US/09966881
 ; Patent No. US20020120960A1

GENERAL INFORMATION:
APPLICANT: Seymour, Graham
Bird, Collin
Medina-Suarez, Rosybel
TITLE OF INVENTION: Genetic control of Fruit Ripening
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zeneca Ag Products Inc.
STREET: 1800 Concord Pike
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/966,881
FILING DATE: 28-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/242,860
FILING DATE: 29-Mar-1999
APPLICATION NUMBER: GB 9618862.8
FILING DATE: 10-SEP-1996
APPLICATION NUMBER: GB 9708366.1
FILING DATE: 25-APR-1997
APPLICATION NUMBER: PCT/GB97/02424
FILING DATE: 08-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschultz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: SEE 50183/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 842 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: U-0115
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-966-881-17
Query Match 17.7%; Score 142.8; DB 10; Length 842;
Best Local Similarity 64.3%; Pred. No. 1,9e-36;
Matches 276; Conservative 0; Mismatches 144; Indels 9; Gaps 5;

325 ATATCAACAGCAGCGCTCGAGATCTCTGGTTATCTGTTGGGTTGAGCAACCG 384
140 AGAAGCTTGAAAGCTGTCCGGGGGCGGAGCTGGGCTCTGTCTATGCGGCACCGGCAATCCG 199
385 ATGACGAGCTGCTGGCGGTGCGACCTGATTGGCATGTCAACAGAAAAAGCTCGCTGAC 444
200 ATGACGAGCTGCTGGCGGTGCGACCTGATTGGCATGTCAACAGCGGAGGCTCGCTGAC 259
445 TGGCGCATTTGGTTGGACGCAACGATANGTGGCGCGGAGGGAATTTTGTGTTGT 504
260 TGGCGCATTTGGTTGGACGCAACGATANGTGGCGCGGAGGGAATTTTGTGTTGT 318
505 GACAGACTCCGGGAGGATATCCCGGATATCTCGCGCGGAGGAGACTAATATACCGG 564
319 GACGACAGCTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 377
565 TCNCTCCANGAAGTTGCCCTCTGTGGATCCCTTTAAACNCAANTGGAATCTCNC 624
378 TCATCC---AGGAGAGAGCGGCTGTGATCATCTTCAAGCGGAGCATGATCATCAGCT- 432

625 NANGAAGACTCCTTTATGACAGCTTTAANACNATGATGAGACNCGTGTCTGTCTCA 684
433 GAAGGAGAGCTATCATCATGACCTCCCAAGACATGACGCGCGGCGGCGGAGCTCA 492
685 CATTCGCAATGGCGGCTGCTGTCACCAACCAATTTCTCCCAACNTCTTCTCCTNCGC 744
493 CATCTCGGCGGCGGCTGATCATCACAC--AGTACGTACCAACATCATCATCACGCGG 550
745 TCCNCTCCG 753
551 TCCACATCC 559
US-09-966-881-14
Sequence 14, Application us/09966881
Patent No. US20020120960A1
GENERAL INFORMATION:
APPLICANT: Seymour, Graham
Bird, Collin
Medina-Suarez, Rosybel
TITLE OF INVENTION: Genetic control of Fruit Ripening
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zeneca Ag Products Inc.
STREET: 1800 Concord Pike
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/966,881
FILING DATE: 28-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/242,860
FILING DATE: 29-Mar-1999
APPLICATION NUMBER: GB 9618862.8
FILING DATE: 10-SEP-1996
APPLICATION NUMBER: GB 9708366.1
FILING DATE: 25-APR-1997
APPLICATION NUMBER: PCT/GB97/02424
FILING DATE: 08-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschultz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: SEE 50183/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: U-069
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-966-881-14
Query Match 16.7%; Score 134.6; DB 10; Length 687;
Best Local Similarity 61.6%; Pred. No. 8.5e-34;
Matches 276; Conservative 0; Mismatches 163; Indels 9; Gaps 5;

325 ATATCAACAGCAGCGCTCGAGATCTCTGGTTATCTGTTGGGTTGAGCAACCG 384
140 AGAAGCTTGAAAGCTGTCCGGGGGCGGAGCTGGGCTCTGTCTATGCGGCACCGGCAATCCG 199


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; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1766
; LENGTH: 1629
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1766

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Query Match	9.2%	Score 74.4;	DB 9;	Length 1629;
Best Local Similarity	57.4%;	Pred. No. 6.3e-14;		
Matches 210; Conservative	0;	Mismatches 146;	Indels 10;	Gaps 5

QY	364	TCGTGCGGGTTCAGGCAACCCGATTCAGACGACTGCTGGCGGT---	GCACCCCTGATTTGGCAT	420
Db	220	TCCTTCCGCTACCGGAAACCCCAATCCGACGATTCTGTGAGATGCAGCCACGACGACTGTCA	279	79
QY	421	GTCAACAGAAAAAGCTCGCTGACTTGGCGGCAATTTGGCTTTGGACGCAACGCNATATANGTGGC	480	
Db	280	ACAACCCGACAAAGACTAGCAGCACTGTGTTCAATCGGCTTCGGACACGGCAACACTCGGAGGC	339	
QY	481	CGCGACGGGGAAATTTGTCGTGTGTGTGACAGACTTCGGGGGACNATGATCCCCGTAAATCTTC	540	
Db	340	AAAAAC-GGCAAGATCTACGTGTGTAATCATCATTCGACAA-CAACCCCAACAAACCAA	397	
QY	541	GCCGGGGAACCTTANATPACCCCGTCNCCANANGAAGTTGCCCCCTCTGGGATCCCTTT	600	
Db	398	CACCAAGGAACTCCGTTACGGCGTATTCAGAA---GAGCACTCTGGATCGTCTTTC	453	
QY	601	AAACNCNANTGGAATATCTCNCCTCANANGAAGAACTCNTATGACAGGTTTAAACNAT	660	
Db	454	TCTTCAAAACATGTCATCAGACT-AAAACAAGACATCATATCAACAGCTACAAAACTT	512	
QY	661	CGATGGACNCGTGTCTCTGTCCACAAATTTGCCAAATGGCGCCTGCTNCCACCAATTTCN	720	
Db	513	AGATGGTGTGGCTCAGCGCTTCACATTAACCGAAAAAGGTTGCTTAATCTCTCCAATACGT	572	
QY	721	TCGCCA	726	
Db	573	TCACCA	578	

RESULT 11
US-09-923-876-4484
; Sequence 4484, Application US/09923876
; Patent No. US20020013958A1
; Sequence 4484, Application US/09923876
; Patent No. US20020013958A1

APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLINGS
FILE REFERENCE: PL-0012-1 CON

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: LENGTH: 277
: TYPE: DNA
: ORGANISM: Zea mays
: FEATURE:
: NAME/KEY: misc-feature
: OTHER INFORMATION: incycle ID No. US20020013958a1 7
: NAME/KEY: unsure
: LOCATION: 2, 63, 118, 122, 186, 199, 263, 267, 270
: OTHER INFORMATION: a, t, c, g, or other
: US-09-923-876-4484

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Query Match	8.5%;	Score 68.4;	DB 10;	Length 277;
Best Local Similarity	61.0%;	Pred. No. 2.8e-12;		
Matches 122;	Conservative	0;	Mismatches 77;	Indels 1;
				Gaps 1

QY	232	GCCGATGCTCCCTTGGAGACAGAGGGCTGTAA	CCCCGGGAGAGAGAAGACCGCATGTGACAC	291
Db	76	GCACGCGCCACGACGAGGGGCGAGGGCCGACG	GTGACGCCGCCGCCGACCGGTGGAGGAT	135
QY	292	CCCCGAGAGAGTTGCTTCGACGGTCTCGATG	ACCATTAATCAACAGACAGCGCTCGCAGATCT	351
Db	136	GCGGAGACGCTGGCCAAACGACGCTCCACGG	GTCCATCAACACACATTCACGCGCCGCGAAT	195
QY	352	CTTGGTTAATCTGTGCTGCGGCTTCAGGCAAC	CCGATCGACAGCACTGCTGGCGGTGCGACCT	411
Db	196	CTCNGGTA-CTGTCGCGCGGAGACAGGCAAC	CCCATCGACGACTGCTGGCGCTGCGACTCG	254
QY	412	GATTGCGATGTCAACAGAA	431	
Db	255	GACTGGCNAACNAACCGAA	274	

RESULT 12
 US-09-938-842A-809
 Sequence 809, Application US/09938842A
 Patent No. US20020160378A1
 GENERAL INFORMATION:
 APPLICANT: Harper, Jeff
 APPLICANT: Kreps, Joel
 APPLICANT: Wang, Xun
 APPLICANT: Zhu, Tong
 TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 TITLE OF INVENTION: SAME, AND METHODS OF USE
 FILE REFERENCE: SCRIPT300-3
 CURRENT APPLICATION NUMBER: US/09/938, 842A
 CURRENT FILING DATE: 2001-08-24
 PRIOR APPLICATION NUMBER: US 60/227, 866
 PRIOR FILING DATE: 2000-08-24
 PRIOR APPLICATION NUMBER: US 60/264, 647
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/300, 111
 PRIOR FILING DATE: 2001-06-22
 NUMBER OF SEQ ID NOS: 5379
 SEQ ID NO 809
 LENGTH: 1185
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 US-09-938-842A-809

Query Match	8.0%;	Score 64.4;	DB 9;	Length 1185;
Best Local Similarity	55.5%;	Pred. No. 1e-10;		
Matches 187; Conservative	0;	Mismatches 140;	Indels 10;	Gaps 4;

QY	379	AACCCATGAGACATCGCTGGGCGGATGCGACCCCTGATTTGGACATGTCACAGAAAAACCTC	438
Db	139	AATCGGCTGAGACCTCGTGTGGGGCGCTCAAGTGTAGCTGGGTGCCAATCGTAAAGACTA	198
QY	439	GCTGACTCGGGCATTTGGCTTTGGACGCAACGCMATANSTGGCCCGGAGCGGAATTTGTT	498
Db	199	GCGGATTTGGCTGTGGATTCGGTT-CATCTACCTTGGGCGGAAAAAGGATTTTATA	257
QY	499	CGTTGTGACAGACTCCGGGGACNATGATCCCGTAATCTCGGCCCGGAACTTANAT	558
Db	258	CGTTGTGACAAACCCCTTAGCAATAGACA-----GAATCTCAACGAGTCTTTGGGCT	313
QY	559	ACCCGCTCNTCCANAGATTGGCCCCCTCTGGGATCCCTTTAAACNCNAAATGGAAATC	618
Db	314	ACGGCGTGATCCAAAGCA---AACCATTTGGGATCACTTCCTGGTAGGAAATGTGATA	369
QY	619	TCACGTNANGAGAGACTCNTTATGACAGCTTTAAACNCNATGCATGAGCAGCNCGTGCT	678
Db	370	ACCCGTGAAA-ATGAGCTCATGTGTCAATATGCTATTAACCACTTGTATGGAGAGGGGCAAA	428
QY	679	CGTTCACATTTGCCAATGGGCGCTGCTGCTATCAGCNCAA	715
Db	429	AGTAGAAATGCGATACGGACCATGATCATCGATTACA	465

